

BAYESIAN DIVERGENCE TIME ESTIMATION

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Český Krumlov, Czech Republic

OUTLINE

Overview of divergence time estimation

- Relaxed clock models – accounting for variation in substitution rates among lineages
 - Dirichlet process prior for lineage-specific rates

break

- Tree priors and fossil calibration

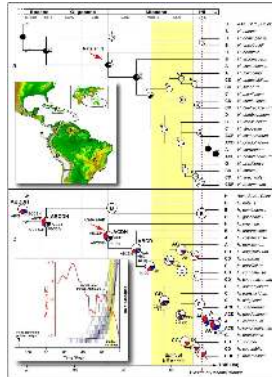
lunch

BEAST Tutorial:

- Walk through: set up BEAST input file in BEAUti and execute BEAST MCMC analysis
- On your own: complete analysis by summarizing output

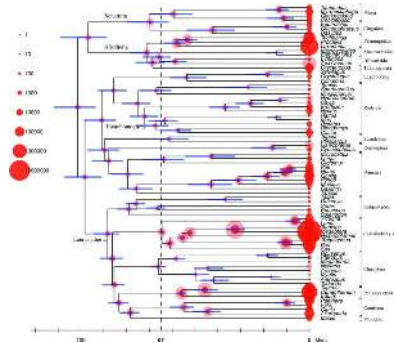
A TIME-SCALE FOR EVOLUTION

- Reconstruct ancestral ranges
- Environmental or geological correlates to diversification
- Morphological character change over time
- Detect shifts in rates of diversification
- Lineage-specific substitution rate



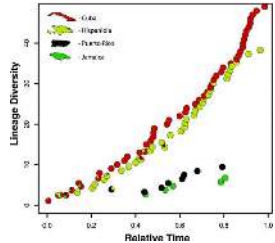
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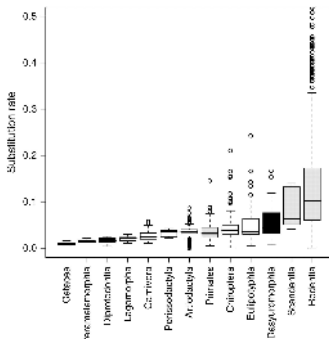
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A TIME-SCALE FOR EVOLUTION

- Reconstruct ancestral ranges
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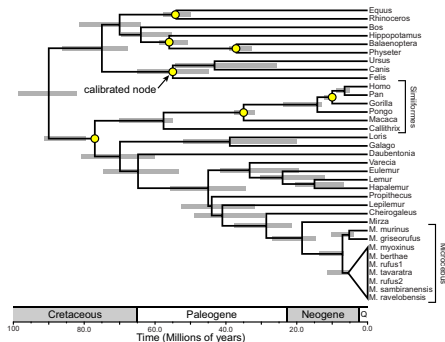
DIVERGENCE TIME ESTIMATION

Goal: Estimate the ages of interior nodes to understand the timing and rates of evolutionary processes

Model how rates are distributed across the tree

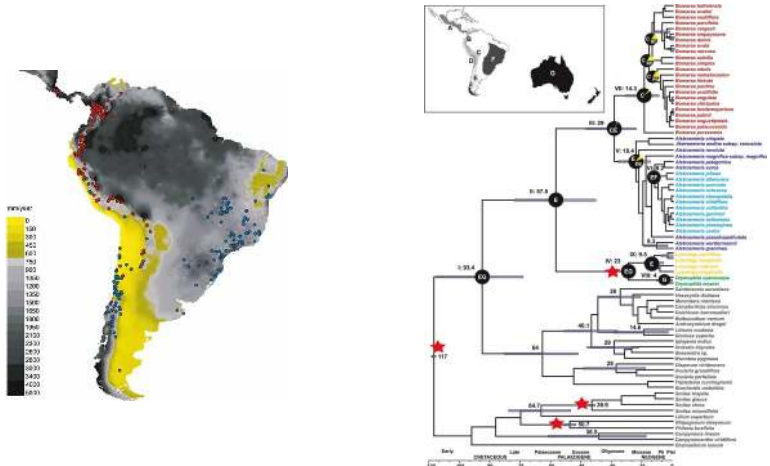
Describe the distribution of speciation events over time

External calibration information for estimates of absolute node times



UNDERSTANDING HISTORICAL BIOGEOGRAPHY

“From East Gondwana to Central America: historical biogeography of the Alstroemeriaceae”



DIVERGENCE TIME ESTIMATION

What about when the fossil record (or other types of calibration information) is poor or absent?

Example: Despite the rich diversity of *Anolis* there are few fossils

There are some amber fossils, but these fossils fall within a narrow time range



DIVERGENCE TIME ESTIMATION

What about when the fossil record is poor or absent?

Model how rates are distributed across the tree

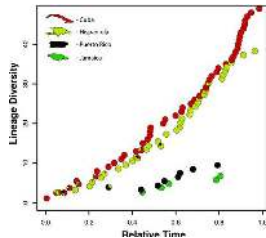
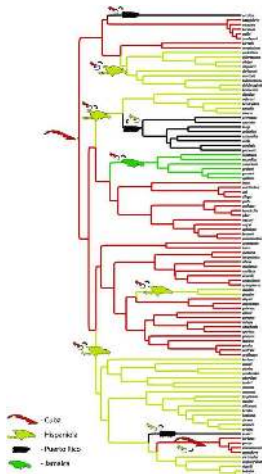
Describe the distribution of speciation events over time

Estimation of relative divergence times



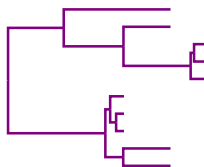
RELATIVE TIMES AND DIVERSIFICATION

“Ecological opportunity and the rate of morphological evolution in the diversification of Greater Antillean Anoles”

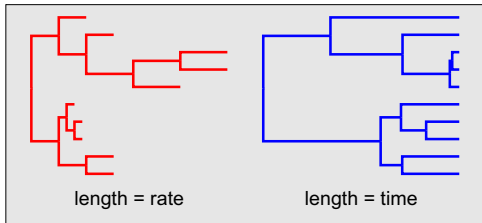


DIVERGENCE TIME ESTIMATION

The expected # of substitutions/site occurring along a branch is the product of the substitution rate and time



length = rate $\times$ time



length = rate

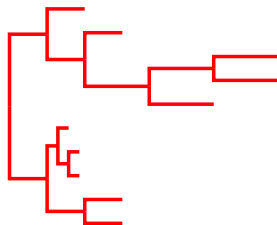
length = time

Methods for dating species divergences estimate the substitution rate and time separately

SUBSTITUTION RATE

Substitution rate: the rate at which mutations are fixed in a population

Depends on: mutation rate, selection, population size, drift

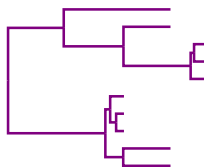


length = subst. rate

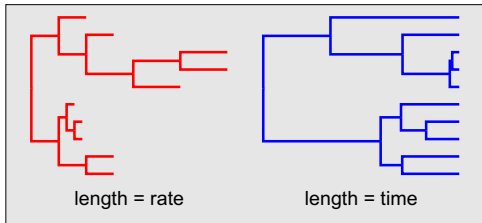
Mutation rate measures the rate at which mutations occur over time and is affected by metabolic rate, generation time, DNA repair efficiency

DIVERGENCE TIME ESTIMATION

The expected # of substitutions/site occurring along a branch is the product of the substitution rate and time



length = rate $\times$ time



length = rate

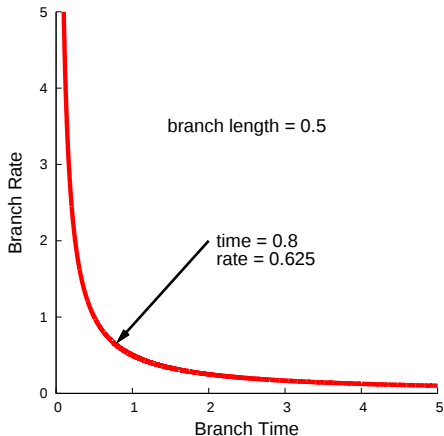
length = time

Methods for dating species divergences estimate the substitution rate and time separately

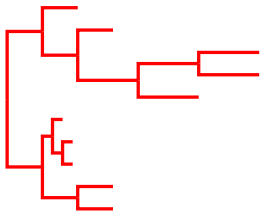
RATES AND TIMES

The sequence data
provide information
about branch length

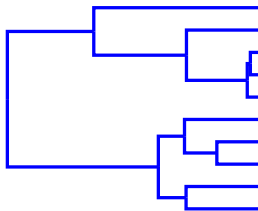
for any possible rate,
there's a time that fits
the branch length
perfectly



BAYESIAN DIVERGENCE TIME ESTIMATION



length = rate



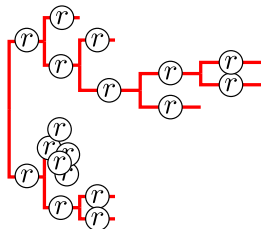
length = time

$$\mathcal{R} = (r_1, r_2, r_3, \dots, r_{2N-2})$$

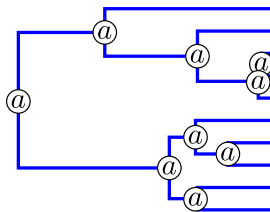
$$\mathcal{A} = (a_1, a_2, a_3, \dots, a_{N-1})$$

$$N = \text{number of tips}$$

BAYESIAN DIVERGENCE TIME ESTIMATION



length = rate



length = time

$$\mathcal{R} = (r_1, r_2, r_3, \dots, r_{2N-2})$$

$$\mathcal{A} = (a_1, a_2, a_3, \dots, a_{N-1})$$

$$N = \text{number of tips}$$

BAYESIAN DIVERGENCE TIME ESTIMATION

Posterior probability

$$f(\mathcal{R}, \mathcal{A}, \theta_{\mathcal{R}}, \theta_{\mathcal{A}}, \theta_s \mid D, \tau)$$

$\mathcal{R}$ Vector of rates on branches

$\mathcal{A}$ Vector of internal node ages

$\theta_{\mathcal{R}}, \theta_{\mathcal{A}}, \theta_s$ Model parameters

D Sequence data

τ Tree topology (assumed known for the moment)

BAYESIAN DIVERGENCE TIME ESTIMATION

$$f(\mathcal{R}, \mathcal{A}, \theta_{\mathcal{R}}, \theta_{\mathcal{A}}, \theta_s | D) = \frac{f(D | \mathcal{R}, \mathcal{A}, \theta_{\mathcal{R}}, \theta_{\mathcal{A}}, \theta_s) f(\mathcal{R}, \mathcal{A}, \theta_{\mathcal{R}}, \theta_{\mathcal{A}}, \theta_s)}{f(D)}$$

$f(D | \mathcal{R}, \mathcal{A}, \theta_{\mathcal{R}}, \theta_{\mathcal{A}}, \theta_s)$

Likelihood

$f(\mathcal{R}, \mathcal{A}, \theta_{\mathcal{R}}, \theta_{\mathcal{A}}, \theta_s)$

Joint prior density

$f(D)$

Marginal probability of the data

BAYESIAN DIVERGENCE TIME ESTIMATION

The likelihood depends on the node times and the rates of evolution, but not on the processes generating the rates and node times

$$f(D \mid \mathcal{R}, \mathcal{A}, \theta_{\mathcal{R}}, \theta_{\mathcal{A}}, \theta_s) = f(D \mid \mathcal{R}, \mathcal{A}, \theta_s)$$

BAYESIAN DIVERGENCE TIME ESTIMATION

Assume that the process governing the ages of nodes operates independently of processes governing mutation, and that the process governing the total rates of substitutions is independent from the mutational parameters that determine relative rates of different substitutions:

$$f(\mathcal{R}, \mathcal{A}, \theta_{\mathcal{R}}, \theta_{\mathcal{A}}, \theta_s) = f(\mathcal{R} \mid \theta_{\mathcal{R}}) f(\mathcal{A} \mid \theta_{\mathcal{A}}) f(\theta_{\mathcal{R}}) f(\theta_{\mathcal{A}}) f(\theta_s)$$

BAYESIAN DIVERGENCE TIME ESTIMATION

After enforcing these assumptions, the posterior distribution of the parameters and hyperparameters can be expressed as:

$$f(\mathcal{R}, \mathcal{A}, \theta_{\mathcal{R}}, \theta_{\mathcal{A}}, \theta_s | D) = \frac{f(D | \mathcal{R}, \mathcal{A}, \theta_s) f(\mathcal{R} | \theta_{\mathcal{R}}) f(\mathcal{A} | \theta_{\mathcal{A}}) f(\theta_{\mathcal{R}}) f(\theta_{\mathcal{A}}) f(\theta_s)}{f(D)}$$

BAYESIAN DIVERGENCE TIME ESTIMATION

Estimating divergence times relies on 2 main elements:

- Branch-specific rates: $f(\mathcal{R} \mid \theta_{\mathcal{R}})$
- Node ages: $f(\mathcal{A} \mid \theta_{\mathcal{A}}, \mathcal{C})$

MODELING RATE VARIATION

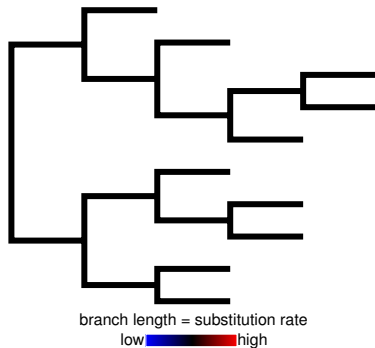
Some models describing lineage-specific substitution rate variation:

- **Global molecular clock** (Zuckerkandl & Pauling, 1962)
- **Local molecular clocks** (Hasegawa, Kishino & Yano 1989; Kishino & Hasegawa 1990; Yoder & Yang 2000; Yang & Yoder 2003, Drummond and Suchard 2010)
- **Compound Poisson process model** (Huelsenbeck, Larget and Swofford 2000)
- **Log-normally distributed autocorrelated rates** (Thorne, Kishino & Painter 1998; Kishino, Thorne & Bruno 2001; Thorne & Kishino 2002)
- **Uncorrelated/independent rates models** (Drummond et al. 2006; Rannala & Yang 2007; Lepage et al. 2007; Heath, Holder, Huelsenbeck 2012)

GLOBAL MOLECULAR CLOCK

The substitution rate is constant over time

All lineages share the same rate



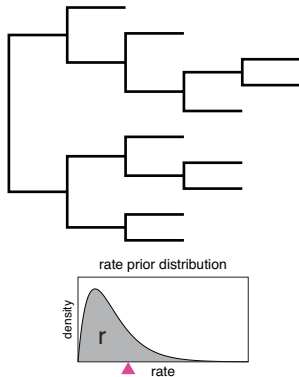
GLOBAL MOLECULAR CLOCK

Assume the clock rate is gamma-distributed

$$\mathcal{R} = (r, r, \dots, r)$$

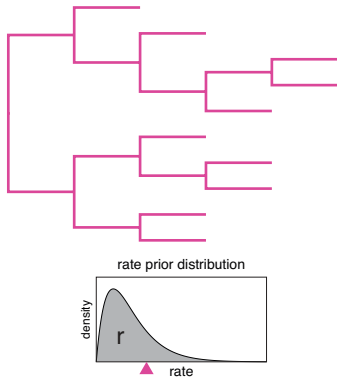
$$r \sim \text{Gamma}(\alpha, \lambda)$$

$$f(\mathcal{R} \mid \theta_{\mathcal{R}}) = f(r \mid \alpha, \lambda)$$



GLOBAL MOLECULAR CLOCK

The sampled rate is applied to every branch in the tree



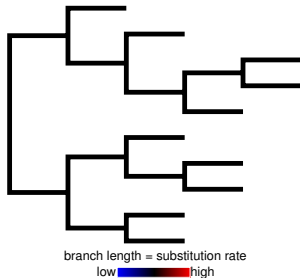
REJECTING THE GLOBAL MOLECULAR CLOCK

Rates of evolution vary across lineages and over time
(and how!)

Mutation rate:

Variation in

- metabolic rate
- generation time
- DNA repair



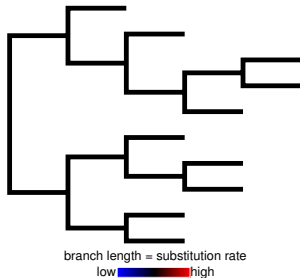
REJECTING THE GLOBAL MOLECULAR CLOCK

Rates of evolution vary across lineages and over time
(and how!)

Fixation rate:

Variability in

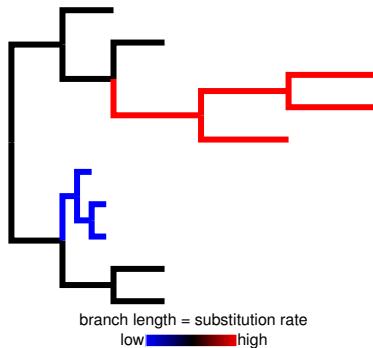
- strength and targets of selection
- population sizes



LOCAL MOLECULAR CLOCKS

Rate shifts occur
infrequently over the tree

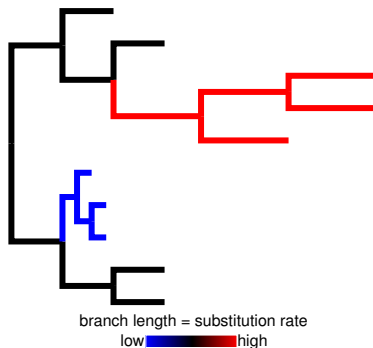
Closely related lineages
have equivalent rates
(clustered by sub-clades)



LOCAL MOLECULAR CLOCKS

Most methods for estimating local clocks required specifying the number and locations of rate changes *a priori*

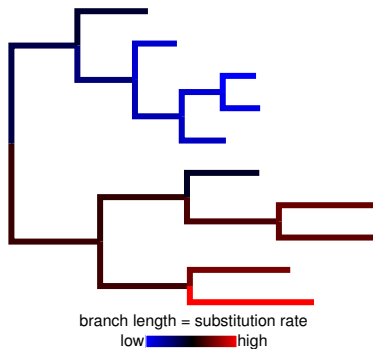
Drummond and Suchard (2010) introduced a Bayesian method that samples over a broad range of possible *random local clocks*



AUTOCORRELATED RATES

Substitution rates evolve gradually over time — closely related lineages have similar rates

The rate at a node is drawn from a lognormal distribution with a mean equal to the parent rate



AUTOCORRELATED RATES

$$\mathcal{R} = (r_1, r_2, \dots, r_{2N-1})$$

$$\sigma^2 = \psi * \Delta t$$

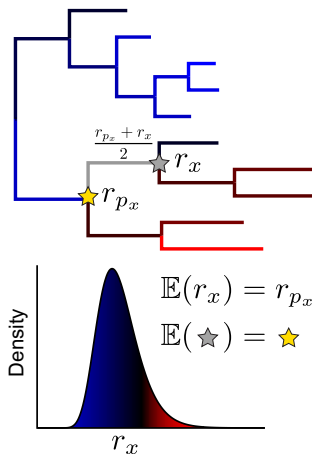
$$\mu = \ln(r_{p_i}) - \frac{\sigma^2}{2}$$

$$r_i \sim \text{Lognormal}(\mu, \sigma^2)$$

$$f(\mathcal{R} \mid \theta_{\mathcal{R}}) = f(\mathcal{R} \mid \psi, \mathcal{A}, r_{root})$$

ψ is the variance parameter

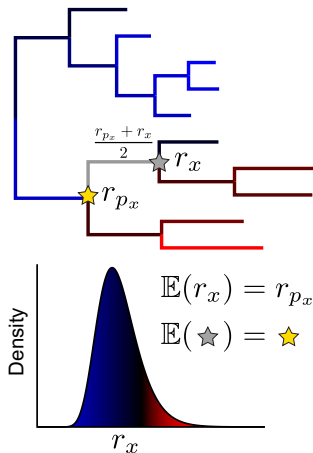
Δt is the difference in time
between the 2 nodes



AUTOCORRELATED RATES

The rate at a node is drawn from a lognormal distribution with a mean equal to the parent rate

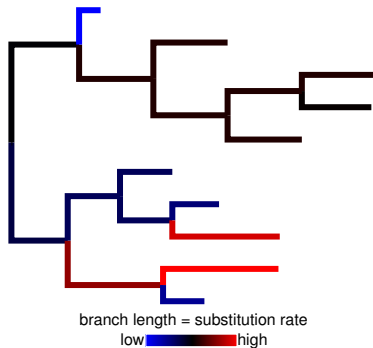
The rate for the branch is equal to the mean of the two subtending nodes



COMPOUND POISSON PROCESS

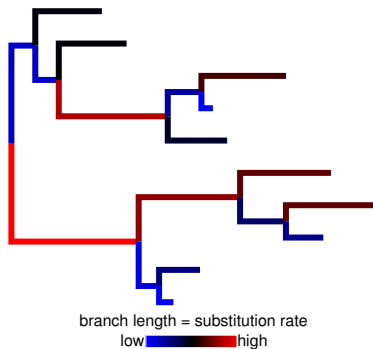
Rate changes occur along lineages according to a point process

At rate-change events, the new rate is a product of the parent's rate and a Γ -distributed multiplier



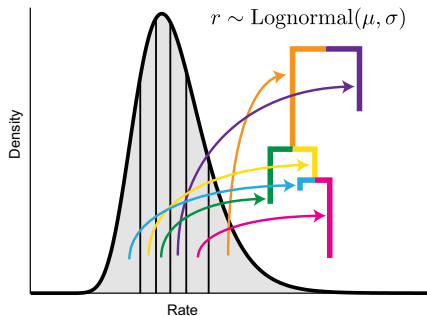
INDEPENDENT/UNCORRELATED RATES

Lineage-specific rates are uncorrelated when the rate assigned to each branch is independently drawn from an underlying distribution

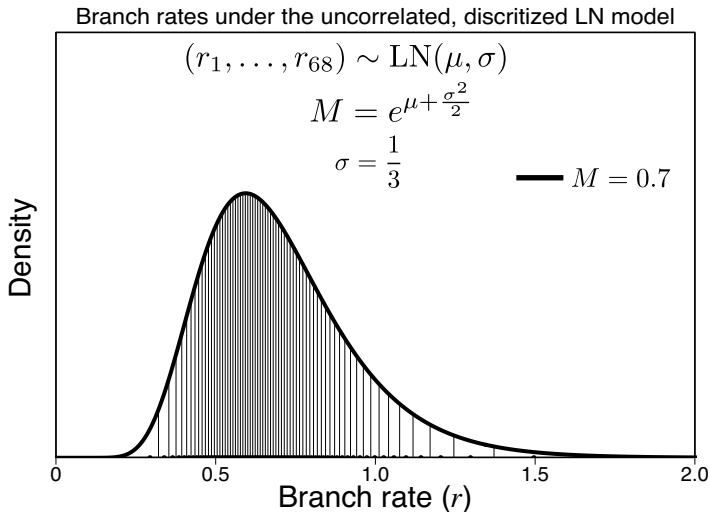


INDEPENDENT/UNCORRELATED RATES

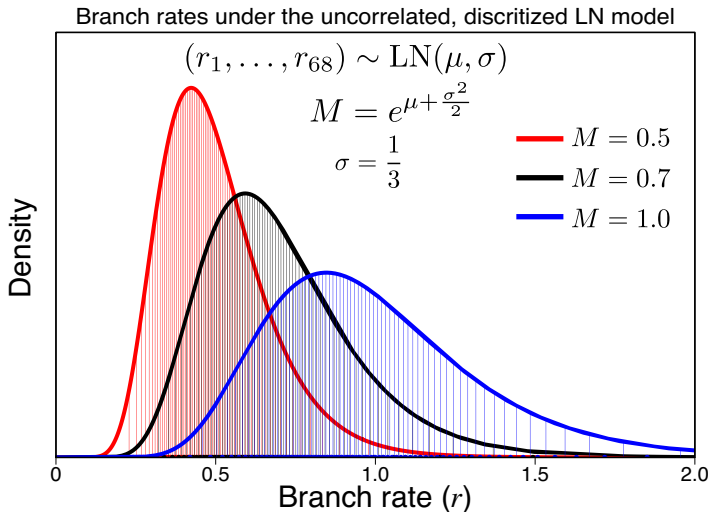
In BEAST, the rates for the branches are drawn from a discretized lognormal distribution



INDEPENDENT/UNCORRELATED RATES



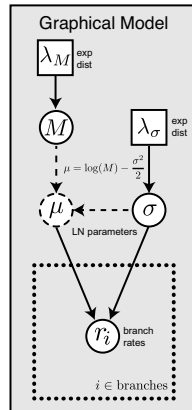
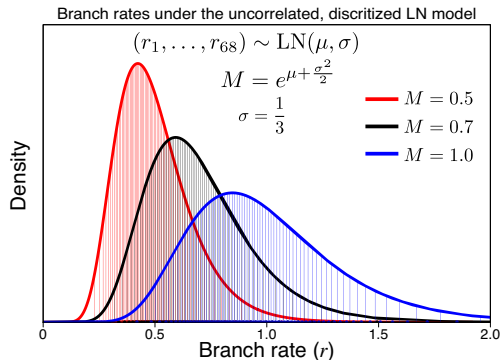
INDEPENDENT/UNCORRELATED RATES



INDEPENDENT/UNCORRELATED RATES

It is necessary to sample the parameters of the base distribution when assuming a discretized model

We can do this using a hierarchical model

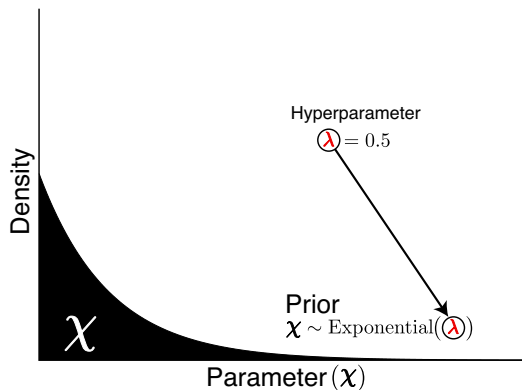


$$\mathbb{E}(M) = \lambda_M^{-1}$$

A HIERARCHICAL BAYESIAN MODEL

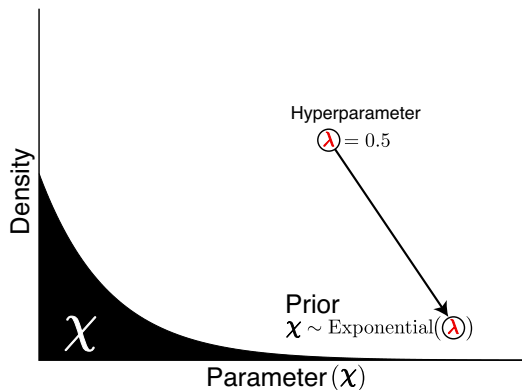
From the bottom up:

The parameter χ is assumed to be drawn from an exponential distribution



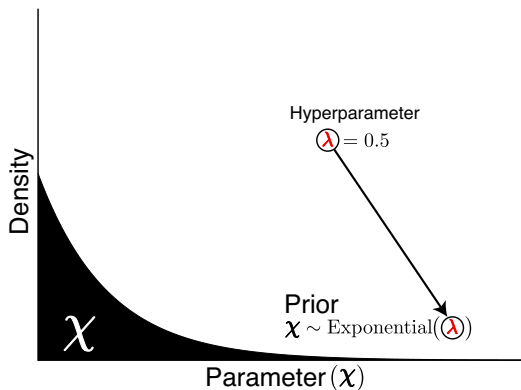
A HIERARCHICAL BAYESIAN MODEL

In Bayesian inference,
a parameter describing
a prior distribution is
called a
hyperparameter



A HIERARCHICAL BAYESIAN MODEL

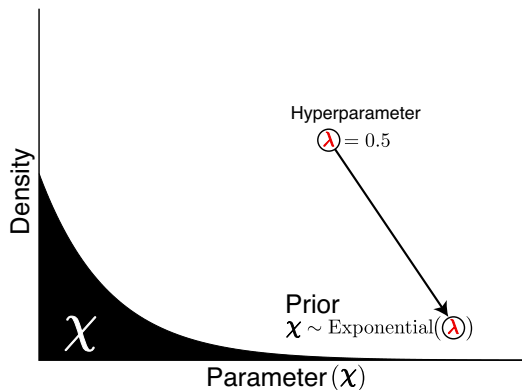
The **exponential** prior on χ has a hyperparameter: λ



A HIERARCHICAL BAYESIAN MODEL

λ represents the **rate** of the exponential distribution

In a non-hierarchical model, the user is required to specify the value of λ

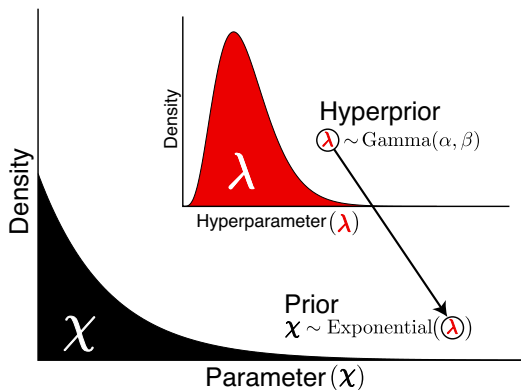


A HIERARCHICAL BAYESIAN MODEL

Hyperprior:

second order prior
placed on a
hyperparameter

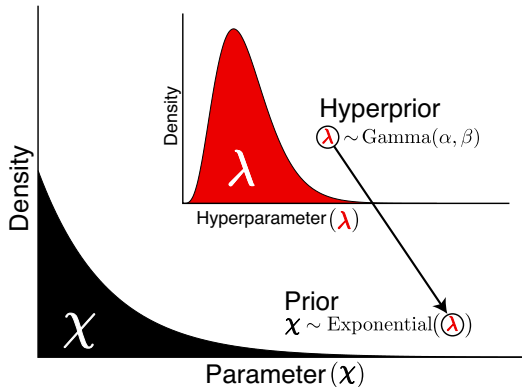
λ becomes a random
variable under the
hierarchical model



A HIERARCHICAL BAYESIAN MODEL

Hyperprior:

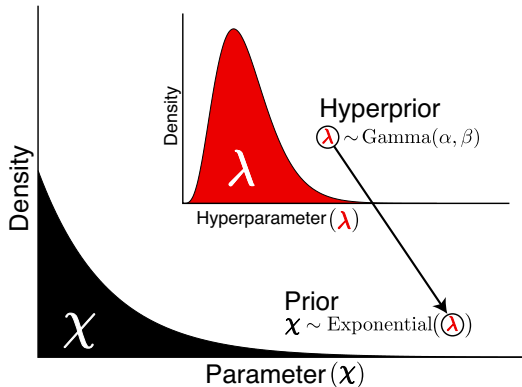
allows for inference under a richer class of models



A HIERARCHICAL BAYESIAN MODEL

Hyperprior:

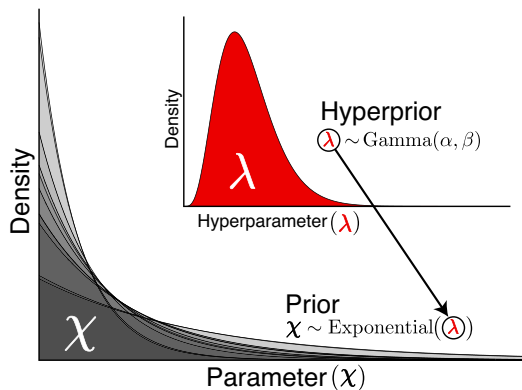
frees the user from the difficulty of specifying the value of λ



A HIERARCHICAL BAYESIAN MODEL

Hyperprior:

values of χ are sampled by MCMC from a mixture of exponential distributions

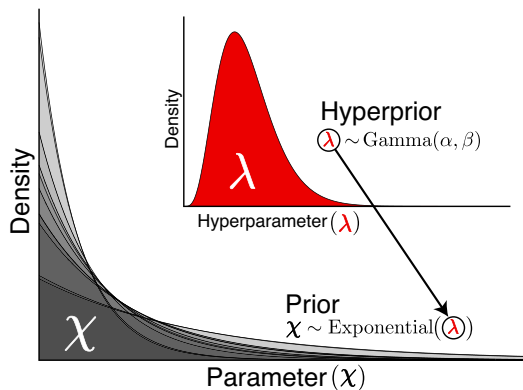


A HIERARCHICAL BAYESIAN MODEL

Hyperprior:

provides estimates of the hyperparameter

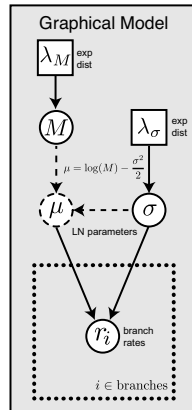
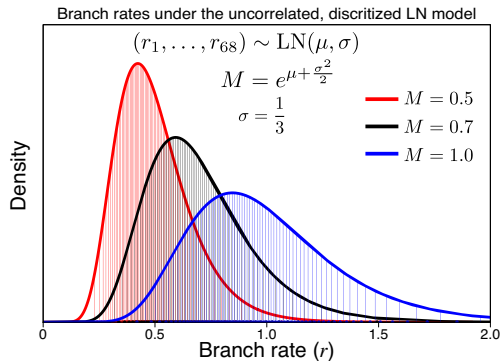
accounts for and quantifies uncertainty in the hyperparameter



INDEPENDENT/UNCORRELATED RATES

It is necessary to sample the parameters of the base distribution when assuming a discretized model

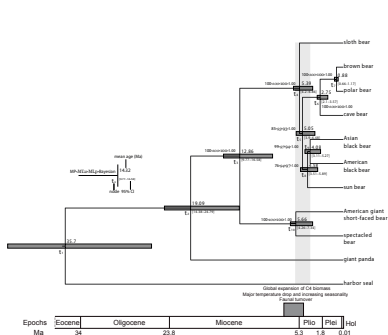
We can do this using a hierarchical model



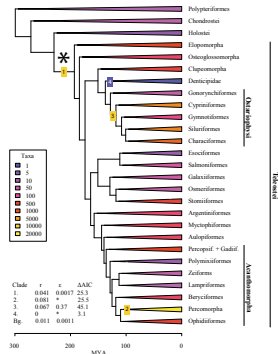
$$\mathbb{E}(M) = \lambda_M^{-1}$$

MODELING RATE VARIATION

Are our models appropriate across all data sets?



Krause et al., 2008. Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. BMC Evol. Biol. 8.



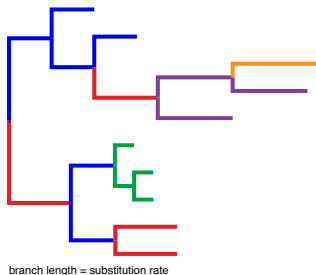
Santini et al., 2009. Did genome duplication drive the origin of teleosts? A comparative study of diversification in ray-finned fishes. BMC Evol. Biol. 9.

THE DIRICHLET PROCESS PRIOR (DPP)

A stochastic process that models data as a mixture of distributions and can identify latent classes present in the data

Branches are assumed to be clustered into distinct substitution rate classes

$$(r_1, \dots, r_{2N-2}) \sim \text{DPP}(\alpha, G_0)$$



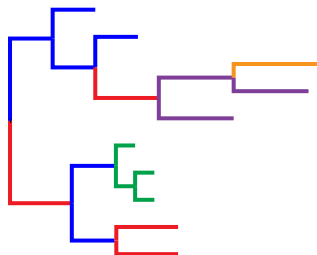
substitution rate classes

THE DIRICHLET PROCESS PRIOR (DPP)

The concentration parameter: α
controls partitioning of branches into specific rate categories

Random variables under the DPP:

- k = the number of rate classes
- the assignment of branches to classes



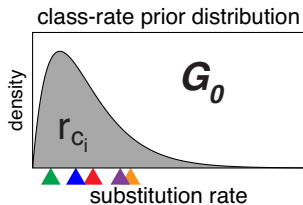
branch length = substitution rate



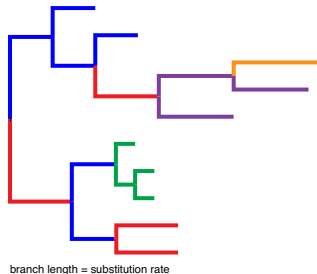
substitution rate classes

THE DIRICHLET PROCESS PRIOR (DPP)

G_0 represents the parametric distribution from which substitution rates are drawn for each category



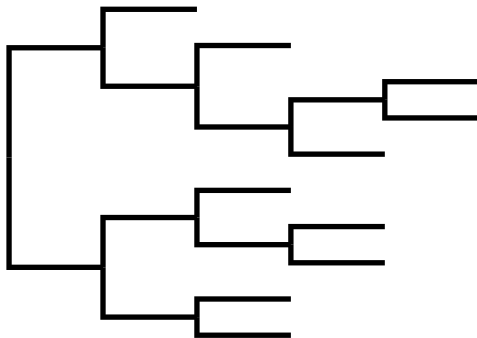
r_{c_i} = the rate value for each class



substitution rate classes

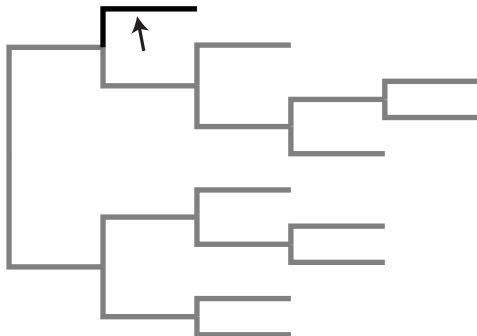
THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate



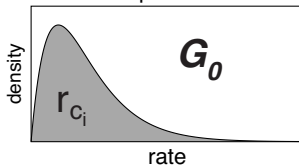
THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate



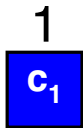
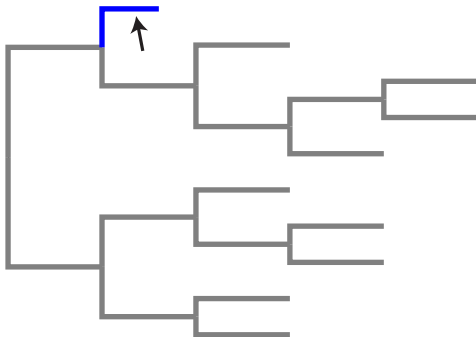
rate classes

class-rate prior distribution



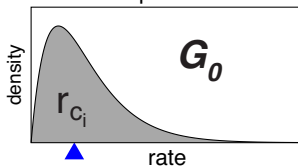
THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate



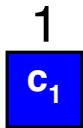
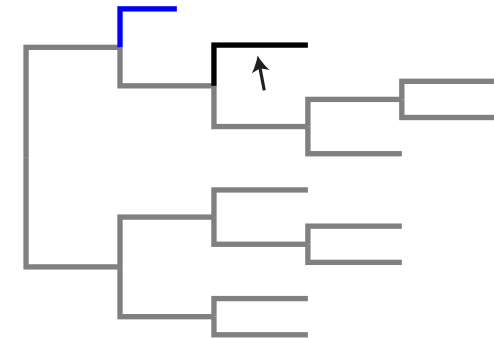
rate classes

class-rate prior distribution

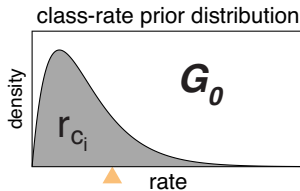


THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate

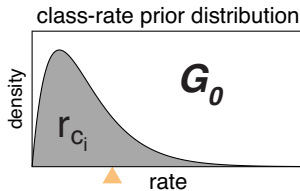
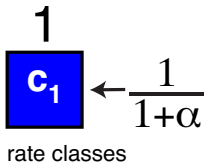
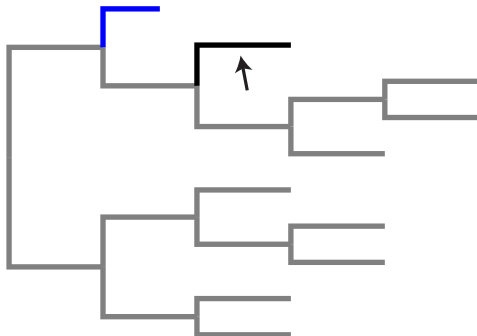


rate classes



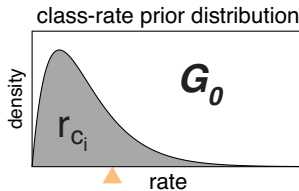
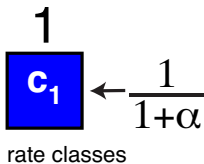
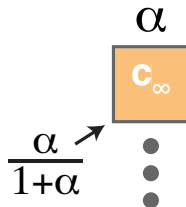
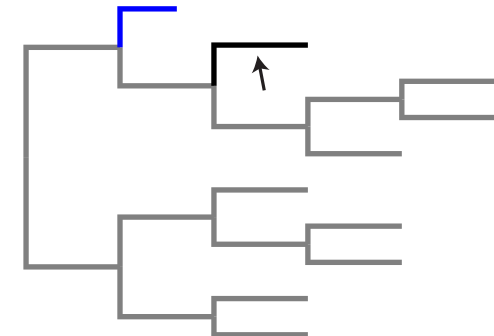
THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate



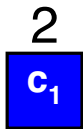
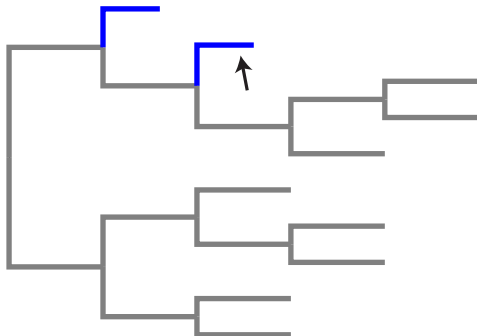
THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate



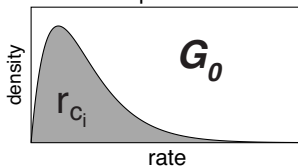
THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate



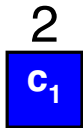
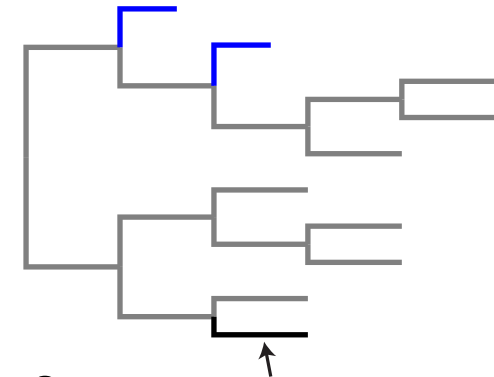
rate classes

class-rate prior distribution

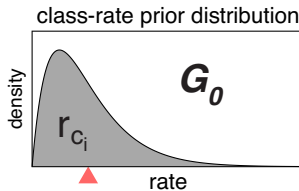


THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate

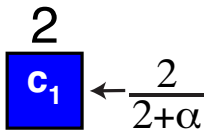
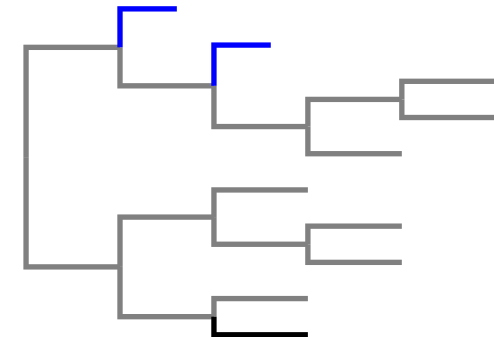


rate classes

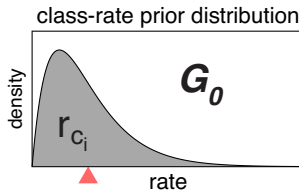
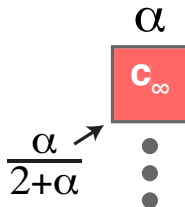


THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate

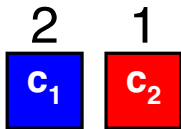
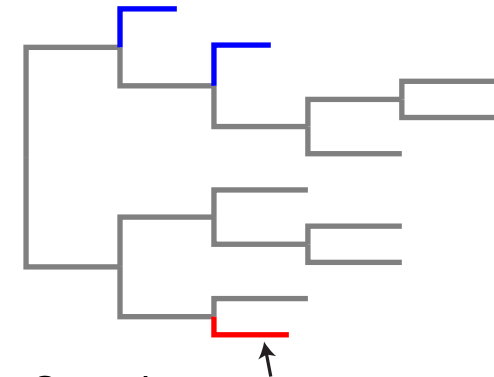


rate classes

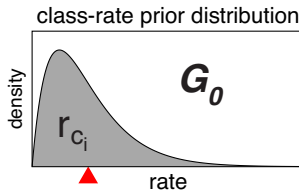


THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate

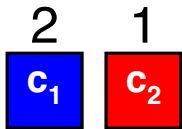
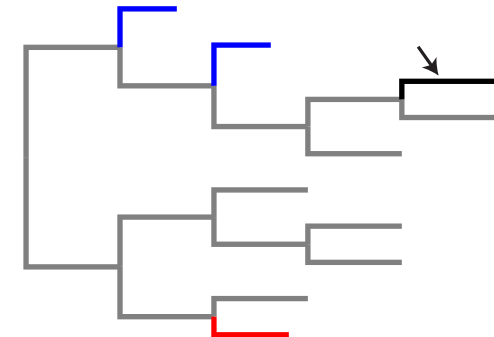


rate classes

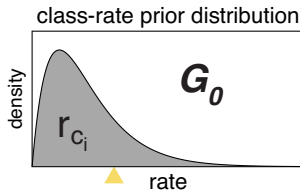


THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate

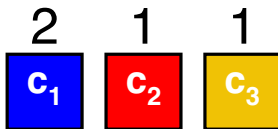
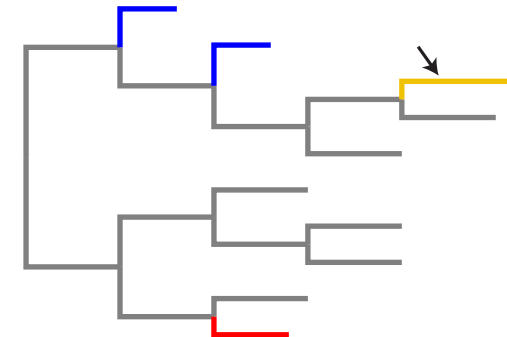


rate classes

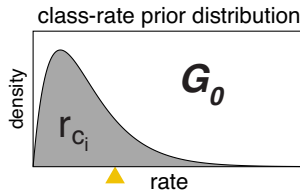


THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate

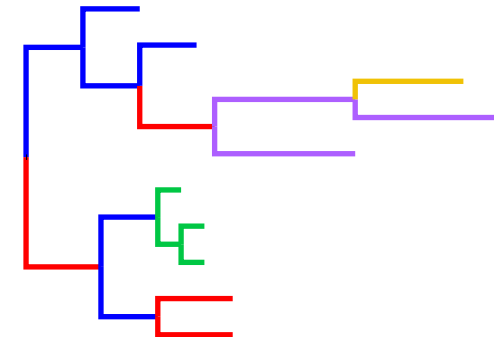


rate classes

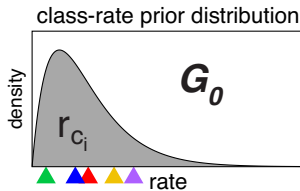


THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate

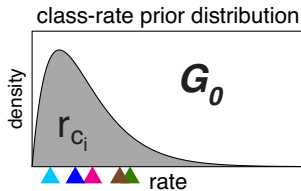
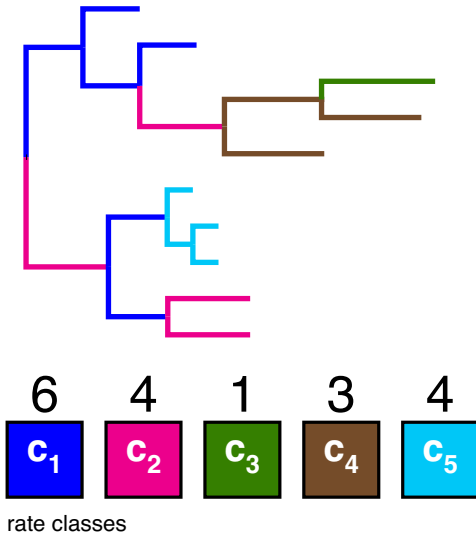


rate classes



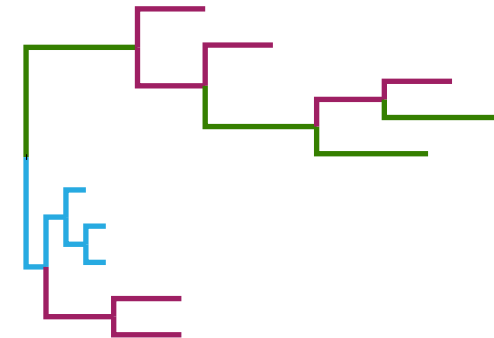
THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate



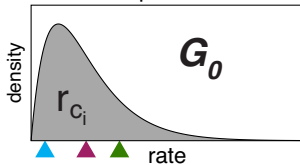
THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate



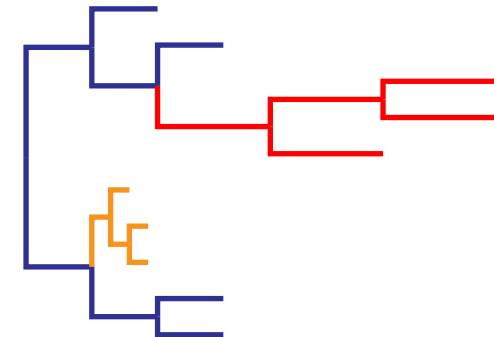
rate classes

class-rate prior distribution



THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate

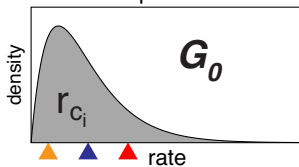


Local molecular
clock



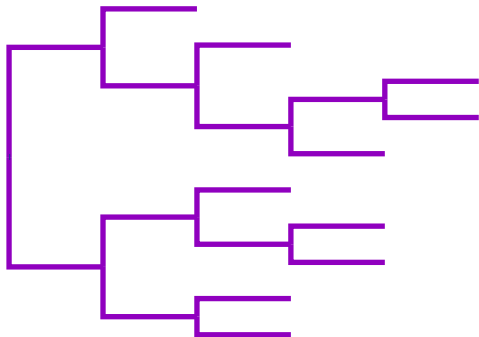
rate classes

class-rate prior distribution



THE DIRICHLET PROCESS PRIOR (DPP)

branch length = substitution rate

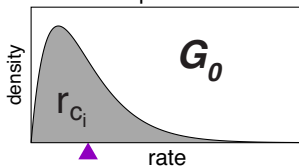


Global molecular
clock

18
C₁

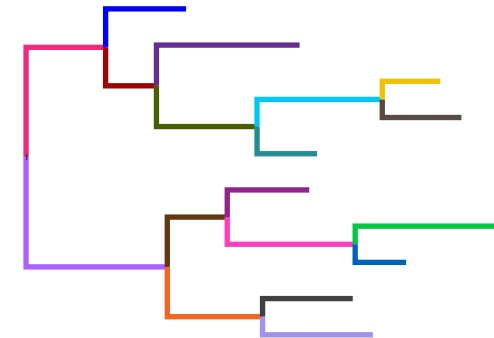
rate classes

class-rate prior distribution

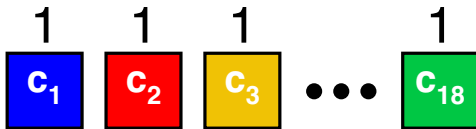


THE DIRICHLET PROCESS PRIOR (DPP)

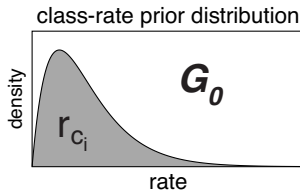
branch length = substitution rate



Independent
rates

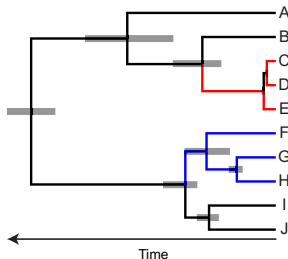


rate classes



BAYESIAN INFERENCE UNDER THE DPP

Current implementation: DPPDiv

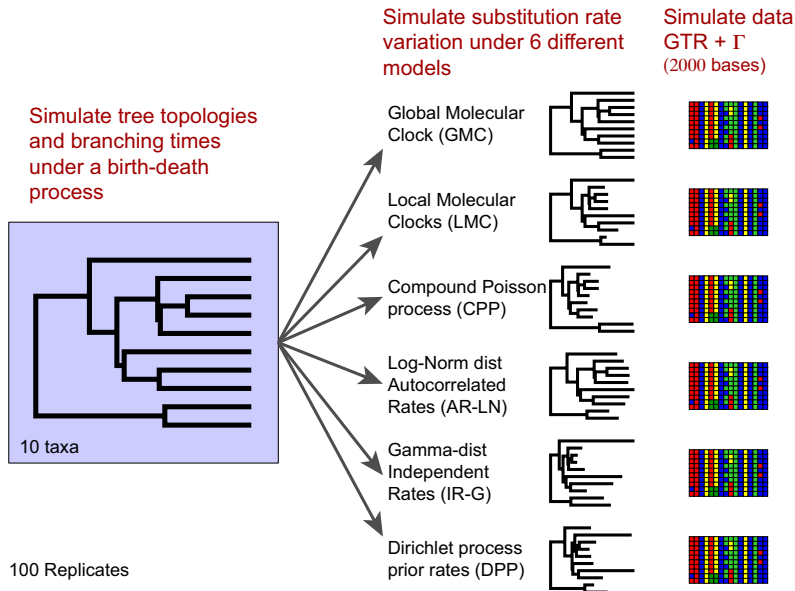


Availability:

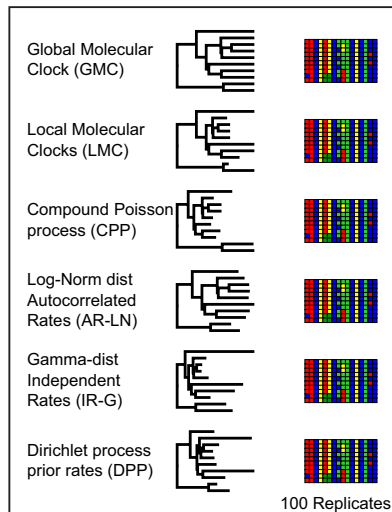
<http://phylo.bio.ku.edu/content/tracy-heath-dppdiv>

*with optimized and parallelized versions by Diego Darriba, Tomáš Flouri, & Alexis Stamatakis

SIMULATIONS: DATA GENERATION



SIMULATIONS: ANALYSIS

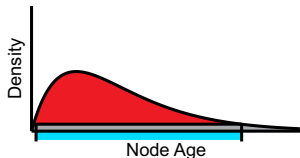
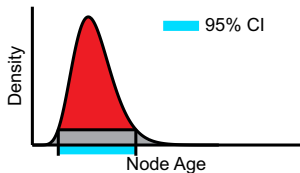
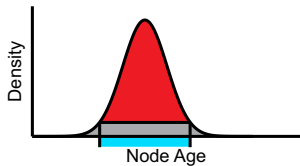


Models of rate variation:

- Dirichlet process prior
 - Gamma-dist hyperprior on α , expected value:
 $E[\alpha] = 1.93$
- Global molecular clock
- Independent rates (Gamma-distributed)

Relative node ages

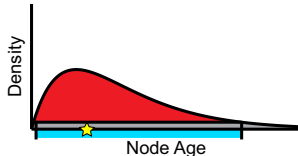
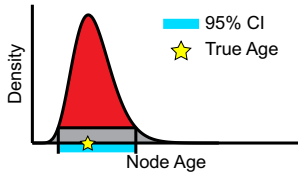
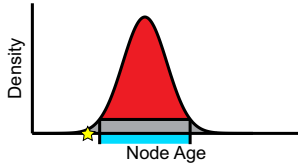
95% CREDIBLE INTERVAL (CI)



A measure of uncertainty

Approximation of the interval containing 95% of the highest posterior density (HPD)

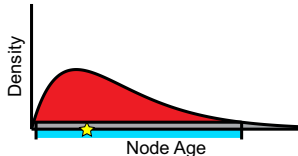
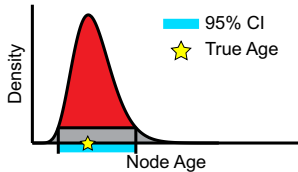
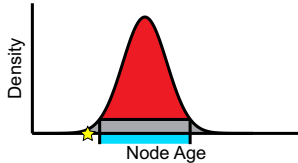
BAYESIAN ANALYSIS OF SIMULATED DATA



Coverage Probability:

The proportion of the time the 95% credible interval (CI) contains the true value is a measure of accuracy

BAYESIAN ANALYSIS OF SIMULATED DATA



Power:

An estimator can have high coverage probability, but reduced power when 95% CIs are very large

BRANCH RATE: ACCURACY

The DPP and Independent Rates models had higher coverage for estimates of branch rates, depending on the simulation model

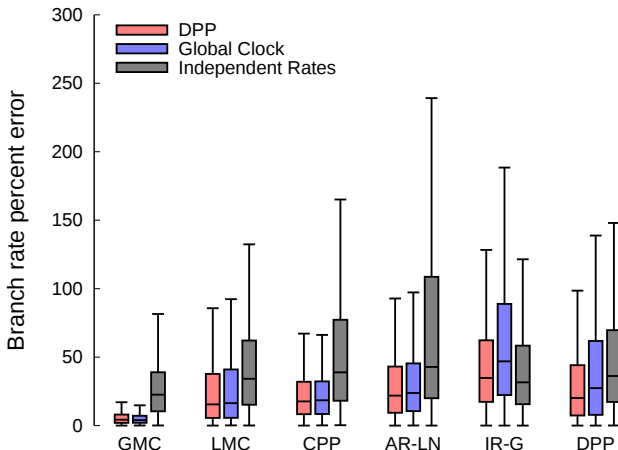
Rate Simulation	Coverage probability*		
	DPP	Independent Rates	Global Clock
<i>GMC</i> – global molecular clock	0.988	0.963	0.920
<i>LMC</i> – local molecular clocks	0.908	0.908	0.398
<i>CPP</i> – compound Poisson	0.807	0.861	0.318
<i>AR-LN</i> – autocorrelated rates	0.801	0.844	0.257
<i>IR-G</i> – independent rates	0.874	0.939	0.126
<i>DPP</i> – Dirichlet process	0.912	0.908	0.292

*Accuracy: proportion of time the 95% credible interval covers the true branch rate

BRANCH RATE: PERCENT ERROR

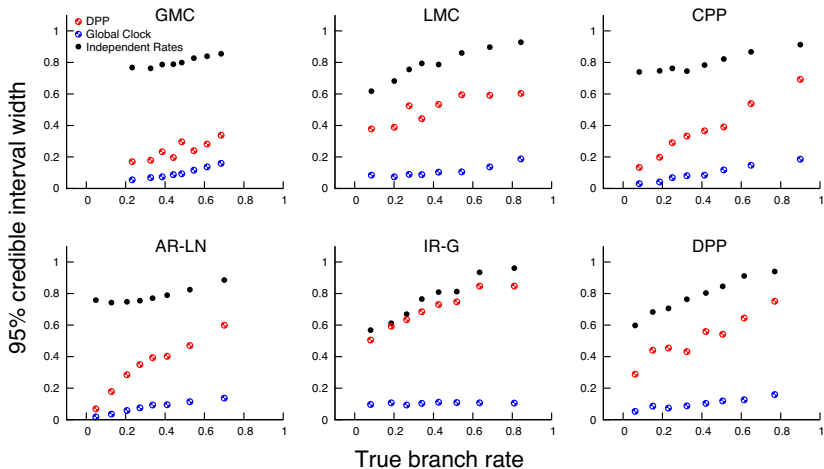
The percent error in mean branch rate estimates

$$\% \text{ Error} = \frac{|\hat{r}_i - r_i|}{r_i} \times 100\%$$



BRANCH RATE: POWER

95% CI size compared to TRUE branch rate



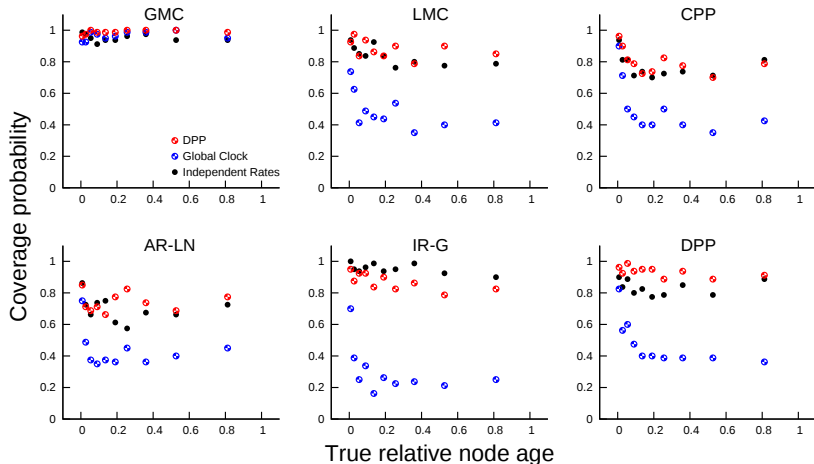
Node Age: Accuracy

Node age estimates under DPP are more accurate compared to an independent rate model and the global molecular clock

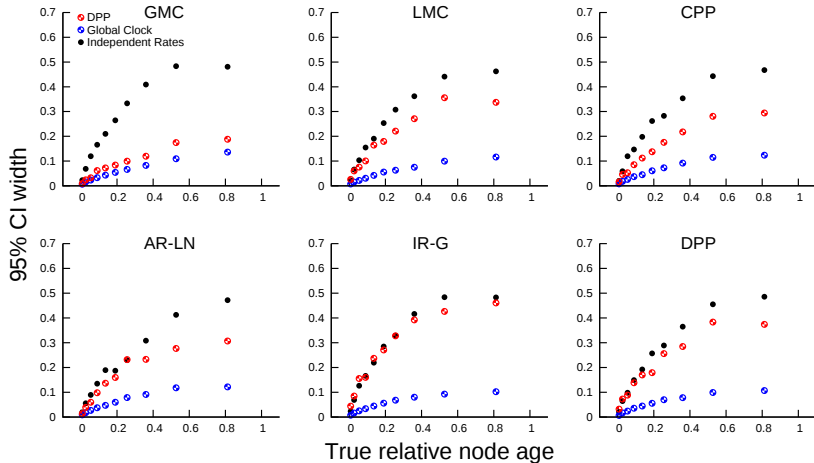
Rate Simulation	Coverage probability*		
	DPP	Independent Rates	Global Clock
<i>GMC</i> – global molecular clock	0.989	0.951	0.965
<i>LMC</i> – local molecular clocks	0.881	0.840	0.485
<i>CPP</i> – compound Poisson	0.801	0.770	0.504
<i>AR-LN</i> – autocorrelated rates	0.743	0.699	0.436
<i>IR-G</i> – independent rates	0.871	0.954	0.303
<i>DPP</i> – Dirichlet process	0.934	0.834	0.479

*Accuracy: proportion of time the 95% credible interval covers the true node age

Node Age: Coverage Probability



Node Age: Power



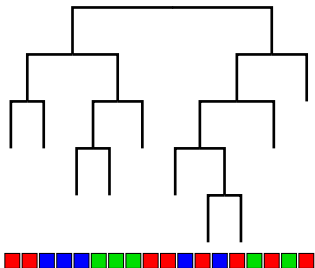
SUMMARIZING MCMC UNDER THE DPP



MEAN PARTITION:

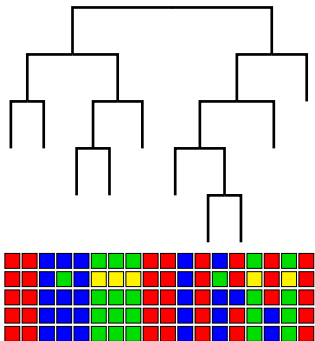
Identified from MCMC
samples under the DPP

SUMMARIZING MCMC UNDER THE DPP



MCMC samples different
branch-partition assignments

SUMMARIZING MCMC UNDER THE DPP



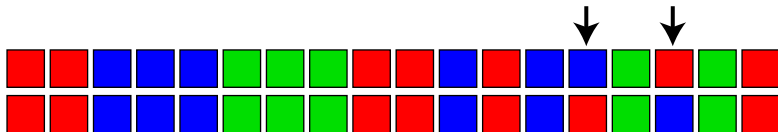
MEAN PARTITION:

Identified from MCMC samples of different branch-partition assignments under the DPP

SUMMARIZING MCMC UNDER THE DPP

PARTITION DISTANCE:

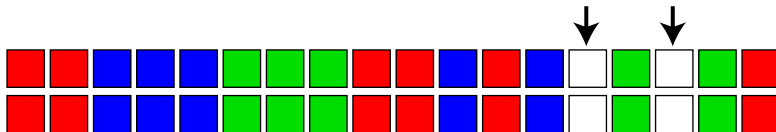
The minimum number of elements that must be removed to make 2 identical partitions



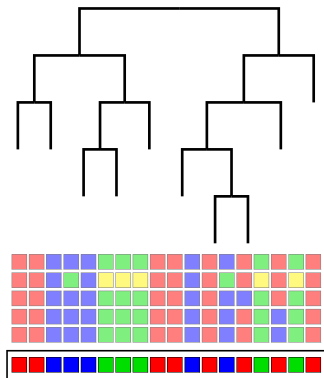
SUMMARIZING MCMC UNDER THE DPP

PARTITION DISTANCE:

The minimum number of elements that must be removed to make 2 identical partitions



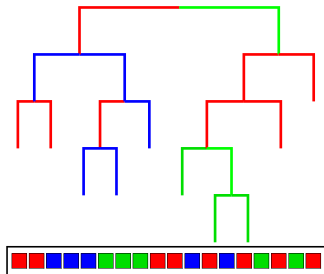
SUMMARIZING MCMC UNDER THE DPP



MEAN PARTITION:

The set of branch-partition assignments that minimizes the sum of squared distances to all of the partition sets sampled by MCMC

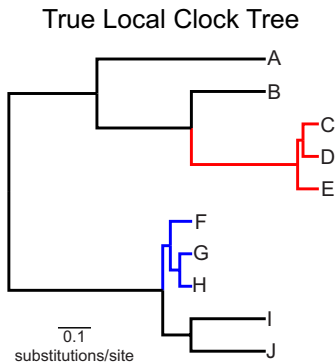
SUMMARIZING MCMC UNDER THE DPP



MEAN PARTITION:

Useful for identifying lineages that may share similar properties

SUMMARIZING MCMC UNDER THE DPP



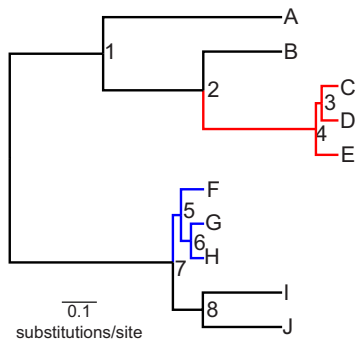
Branch lengths generated under a local molecular clock (LMC)

3 rate categories
(substitutions/site* time^{-1}):

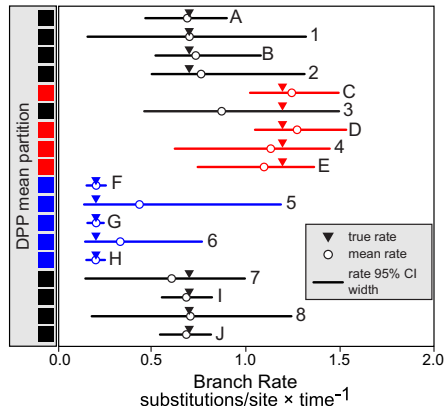
- **0.2**
- **0.7**
- **1.2**

SUMMARIZING MCMC UNDER THE DPP

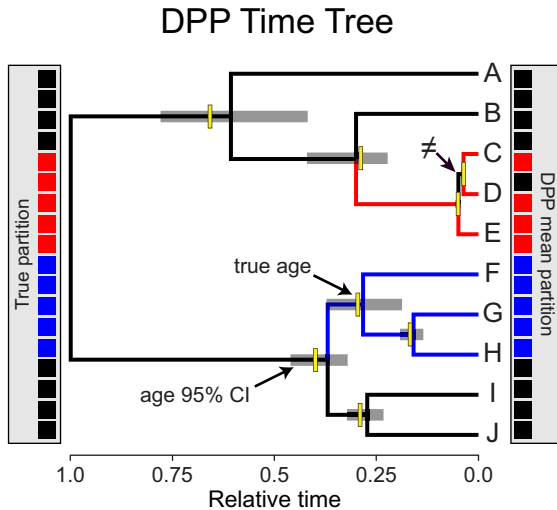
True Local Clock Tree



DPP Estimated Branch Rate



SUMMARIZING MCMC UNDER THE DPP

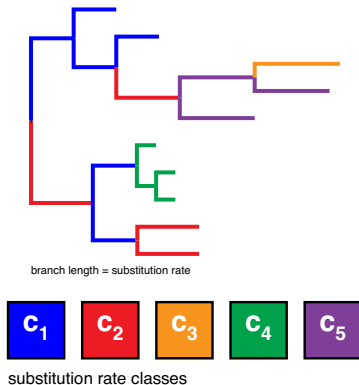


LINEAGE-SPECIFIC SUBSTITUTION RATES

DPP provides robust estimates of branch-rate and node-age without significant loss in power

The flexibility of the DPP allows it to encompass different branch-wise models of substitution rate variation

Including cases in which distant branches have equivalent (or nearly equivalent) rates

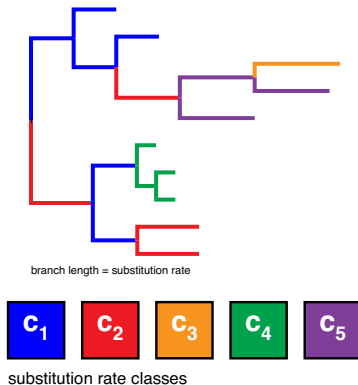


LINEAGE-SPECIFIC SUBSTITUTION RATES

DPP provides robust estimates of branch-rate and node-age without significant loss in power

The mean branch partition found under the DPP allows for the identification of latent classes

Efficient MCMC implementations



let's take a break...

BAYESIAN DIVERGENCE TIME ESTIMATION

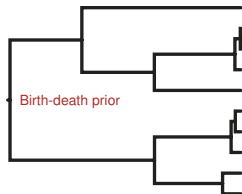
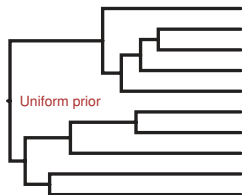
Estimating divergence times relies on 2 main elements:

- Branch-specific rates: $f(\mathcal{R} \mid \theta_{\mathcal{R}})$
- Node ages: $f(\mathcal{A} \mid \theta_{\mathcal{A}}, \mathcal{C})$

PRIORS ON NODE TIMES

Relaxed clock Bayesian analyses require a prior distribution on node times

Uniform prior: the time at a given node has equal probability across the interval between the time of the parent node and the time of the oldest daughter node

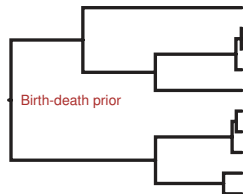
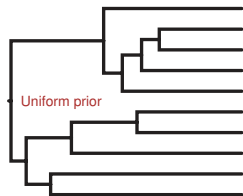


PRIORS ON NODE TIMES

Relaxed clock Bayesian analyses require a prior distribution on node times

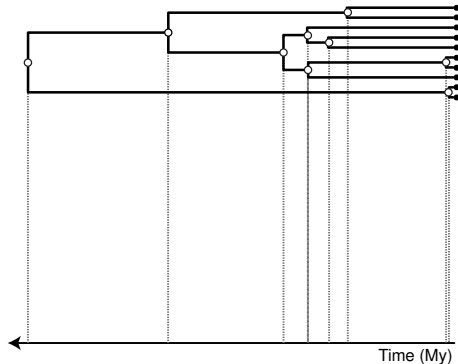
Birth-death prior: node times are sampled from a stochastic process with parameters for speciation, $\mathcal{S}$, and extinction, $\mathcal{E}$, (and in some cases taxon sampling)

$$f(\mathcal{A} | \mathcal{S}, \mathcal{E})$$



FOSSIL CALIBRATION

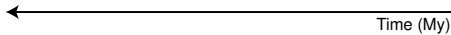
Fossil and geological data can be used to estimate the absolute ages of ancient divergences



FOSSIL CALIBRATION



The ages of extant taxa
are known



FOSSIL CALIBRATION

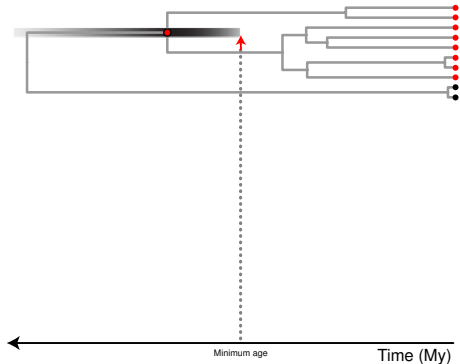


Fossil taxa are assigned to monophyletic clades



FOSSIL CALIBRATION

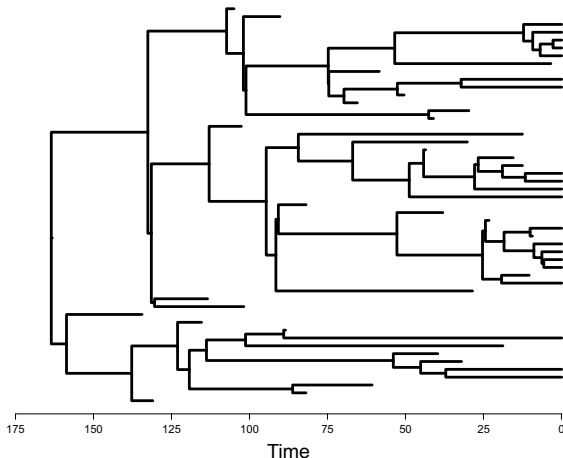
Fossil taxa are assigned to monophyletic clades and constrain the age of the MRCA



MODELING BRANCHING PROCESSES

Assume constant
rates of
speciation ($\mathcal{S}$)
and extinction ($\mathcal{E}$)

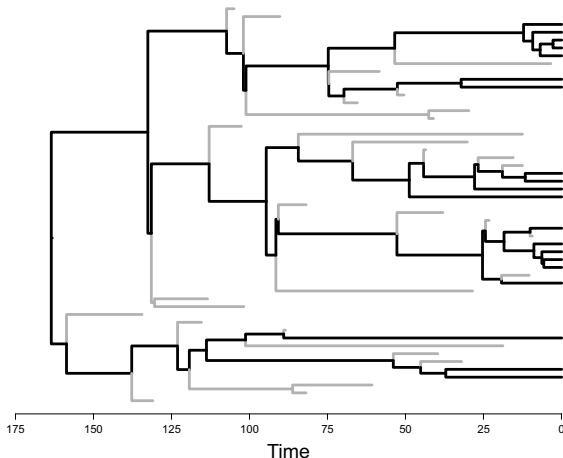
(20 extant taxa)



MODELING BRANCHING PROCESSES

Assume constant
rates of
speciation ($\mathcal{S}$)
and extinction ($\mathcal{E}$)

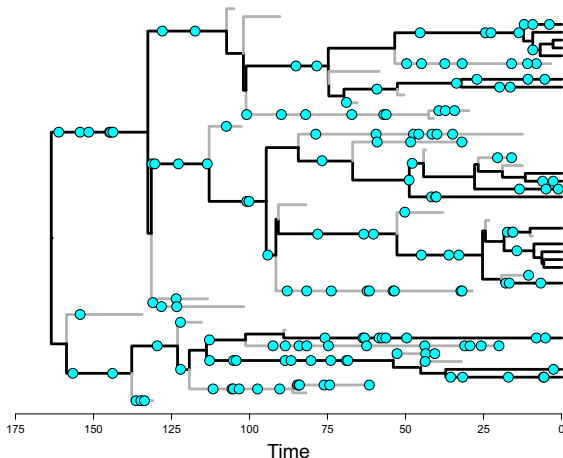
(20 extant taxa)



MODELING TAPHONOMIC PROCESSES

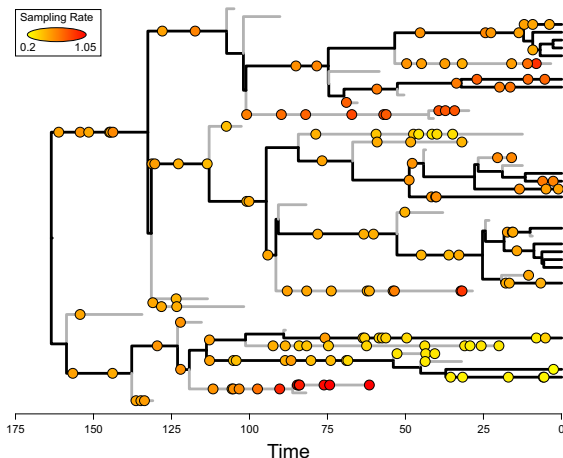
Fossilization events were generated according to a Poisson process

this example has 162 fossilization events



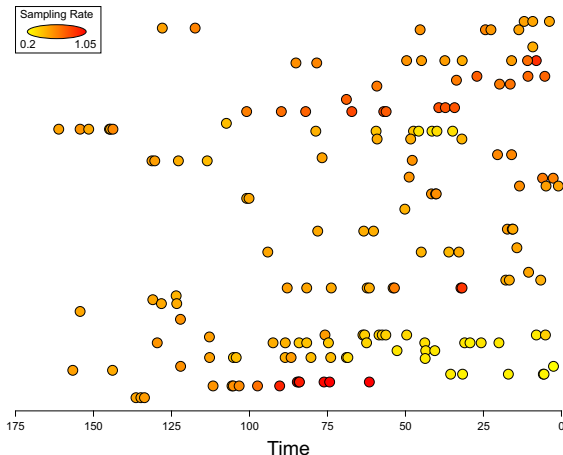
MODELING TAPHONOMIC PROCESSES

The fossil sampling rate was evolved under an autocorrelated Brownian motion model



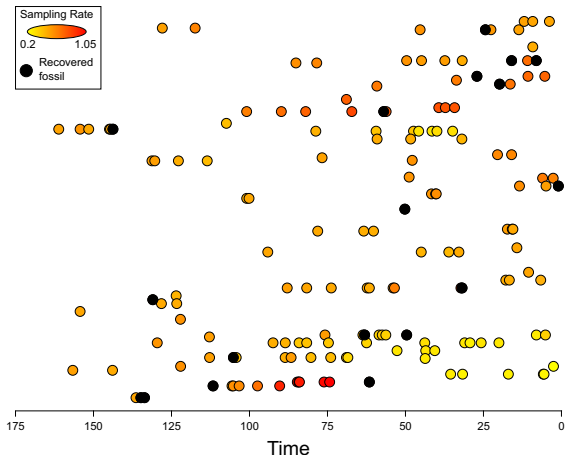
MODELING TAPHONOMIC PROCESSES

The fossil
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Brownian motion
model



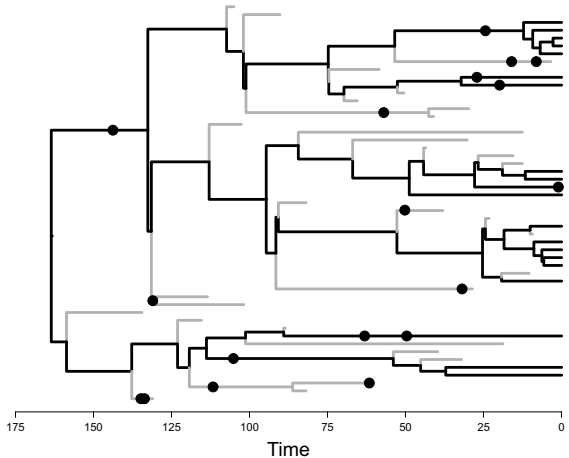
MODELING TAPHONOMIC PROCESSES

18 fossils were
“recovered” in
proportion to
their sampling
rates



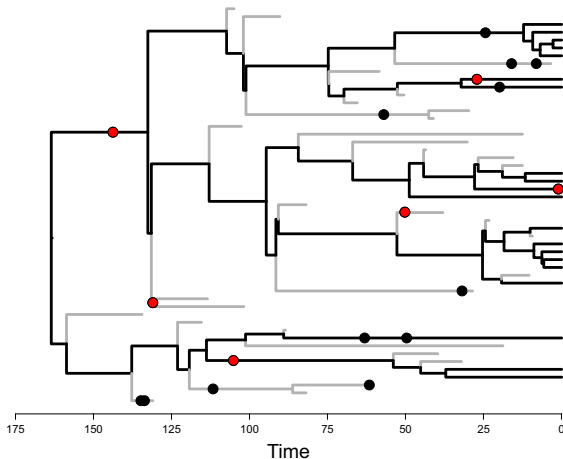
RECOVERED FOSSILS

Assume we
know the true
phylogenetic
placement of the
recovered fossils



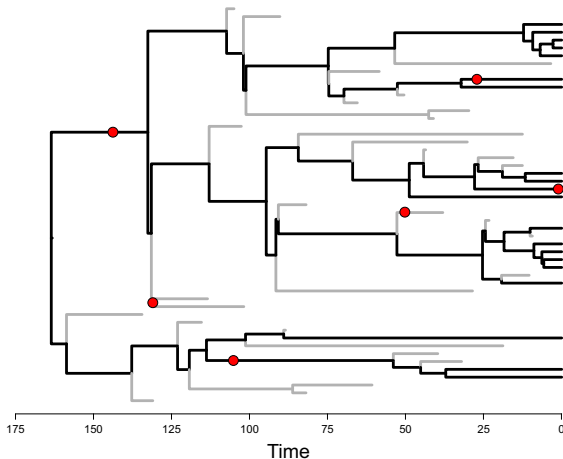
CALIBRATION FOSSILS

Only the oldest fossil assigned to a given node can be used for calibration



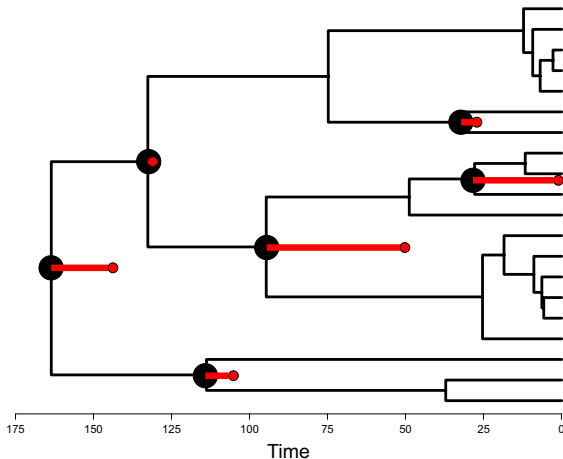
CALIBRATION FOSSILS

Only the oldest fossil assigned to a given node can be used for calibration



CALIBRATION FOSSILS

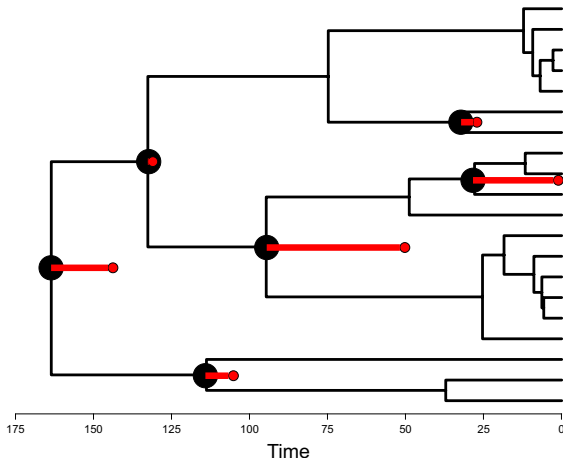
Only the oldest fossil assigned to a given node can be used for calibration



CALIBRATION FOSSILS

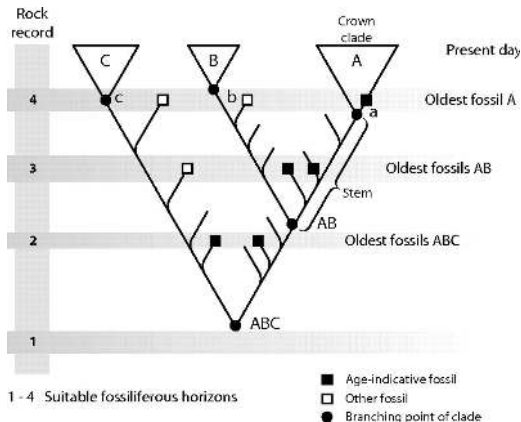
Taphonomic bias

- disparity in fossilization and preservation
- geographical distribution
- recovery bias
- identification



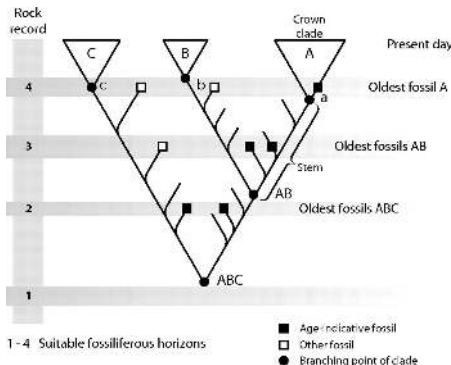
ASSIGNING FOSSILS TO CLADES

Misplaced fossils can affect node age estimates throughout the tree – if the fossil is older than its presumed MRCA



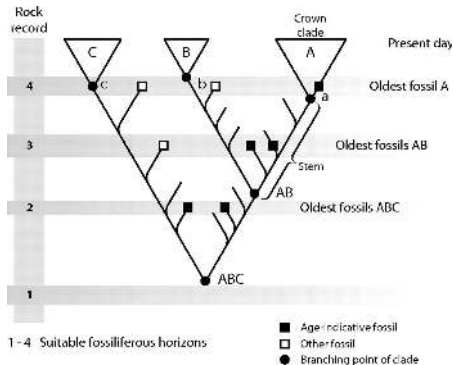
ASSIGNING FOSSILS TO CLADES

Crown clade: all living species and their most-recent common ancestor (MRCA)



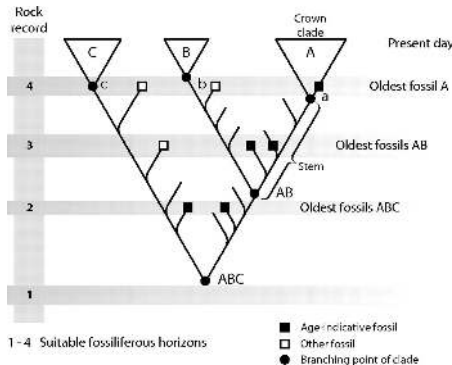
ASSIGNING FOSSILS TO CLADES

Stem lineages:
purely fossil forms
that are closer to
their descendant
crown clade than
any other crown
clade



ASSIGNING FOSSILS TO CLADES

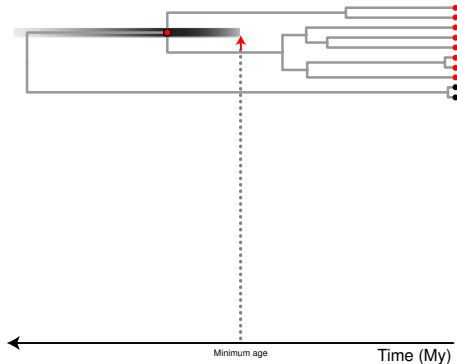
Fossiliferous horizons: the sources in the rock record for relevant fossils



FOSSIL CALIBRATION

Age estimates from fossils can provide **minimum** time constraints for internal nodes

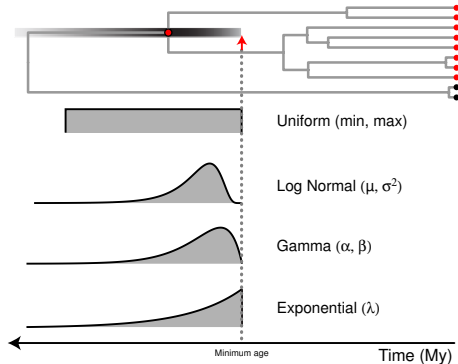
Reliable **maximum** bounds are typically unavailable



PRIOR DENSITIES ON CALIBRATED NODES

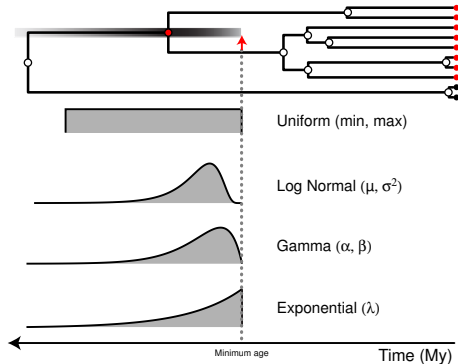
Parametric distributions are typically off-set by the age of the oldest fossil assigned to a clade

These prior densities do not (necessarily) require specification of maximum bounds



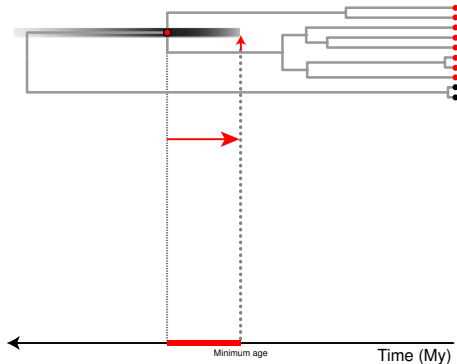
PRIOR DENSITIES ON CALIBRATED NODES

Describe the waiting time between the divergence event and the age of the oldest fossil



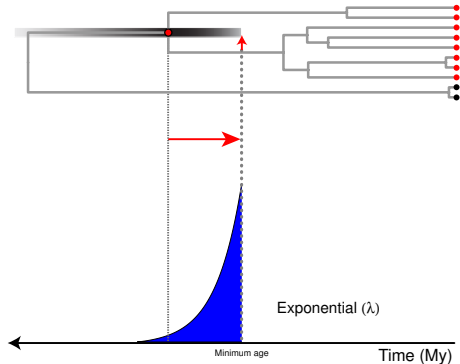
PRIOR DENSITIES ON CALIBRATED NODES

Describe the waiting time between the divergence event and the age of the oldest fossil



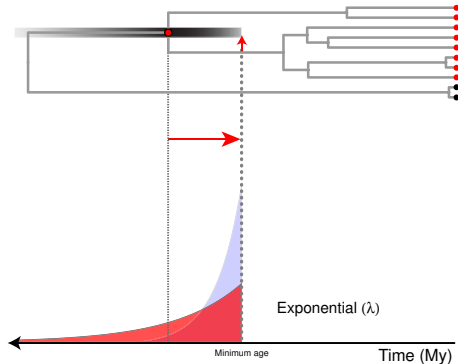
PRIOR DENSITIES ON CALIBRATED NODES

Overly **informative** priors
can bias node age
estimates to be too young



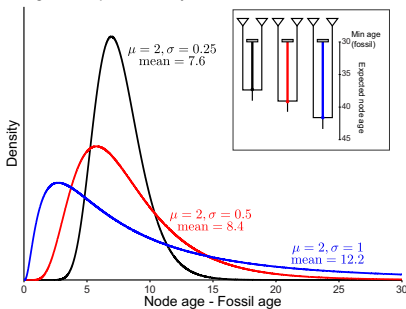
PRIOR DENSITIES ON CALIBRATED NODES

Uncertainty in the age of the MRCA of the clade relative to the age of the fossil may be better captured by **vague** prior densities

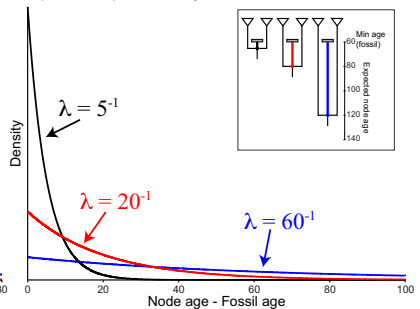


PRIOR DENSITIES ON CALIBRATED NODES

Lognormal prior density

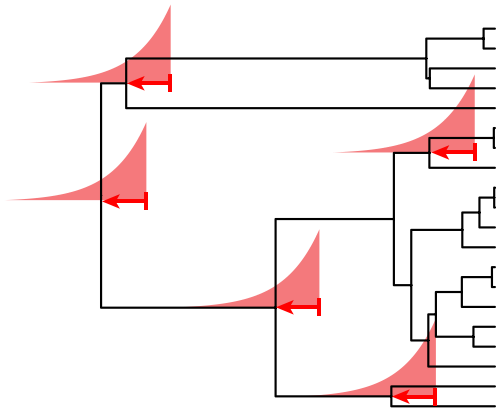


Exponential prior density



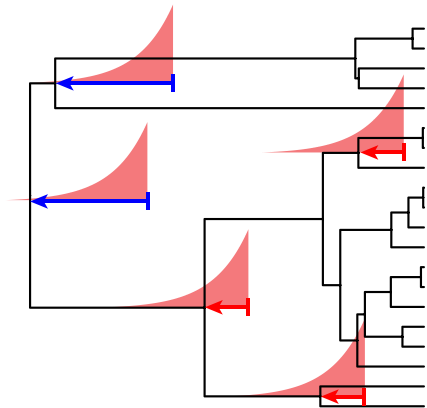
PRIORS ON MULTIPLE CALIBRATIONS

It is unlikely that multiple fossil calibrations can be characterized by a single prior density



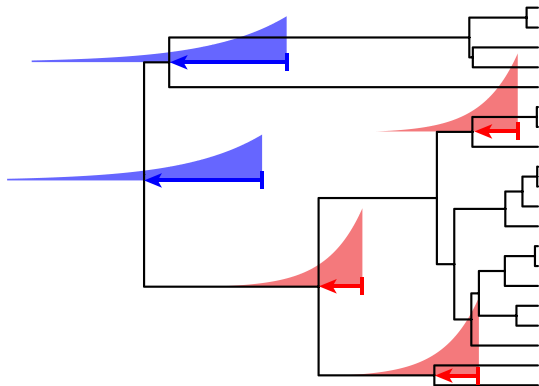
PRIORS ON MULTIPLE CALIBRATIONS

An appropriate prior for some nodes can also be an overly **informative** prior for other nodes



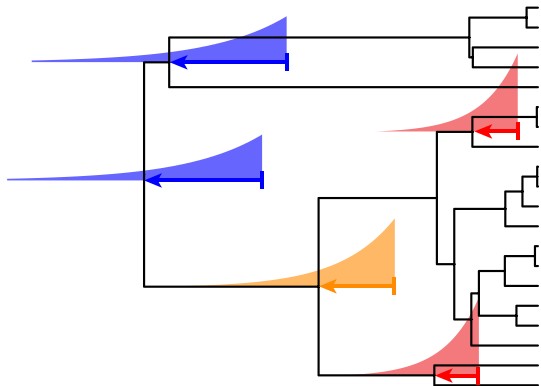
PRIORS ON MULTIPLE CALIBRATIONS

Our knowledge of the fossil and rock records indicate that there is variation in the precision of geological data as minimum age constraints



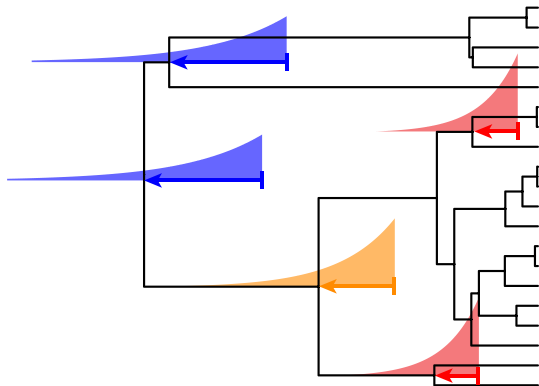
PRIORS ON MULTIPLE CALIBRATIONS

Uncertainty in the time difference can be better captured by **vague** prior densities

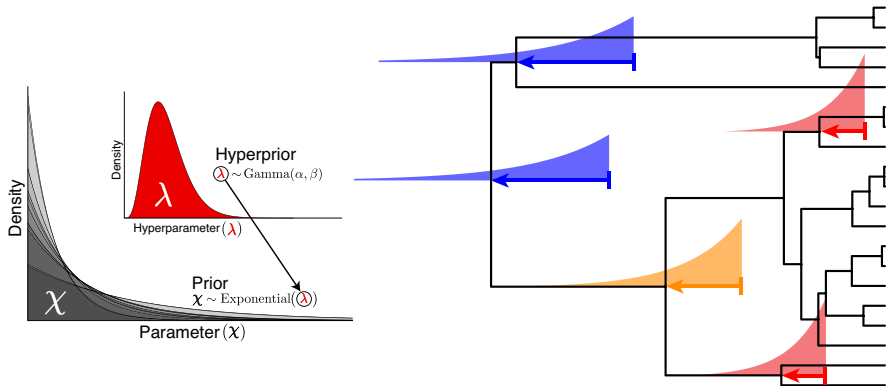


PRIORS ON MULTIPLE CALIBRATIONS

Specifying appropriate prior densities for a range of minimum age constraints is a challenge for most molecular biologists



PRIORS ON MULTIPLE CALIBRATIONS

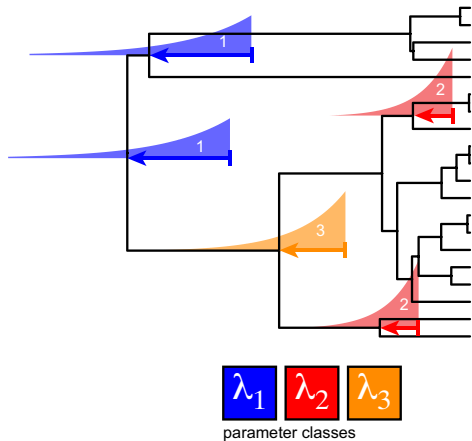


HYPERPRIOR ON CALIBRATED NODES

Dirichlet process prior on rate-parameters of exponential prior densities on multiple calibrated nodes

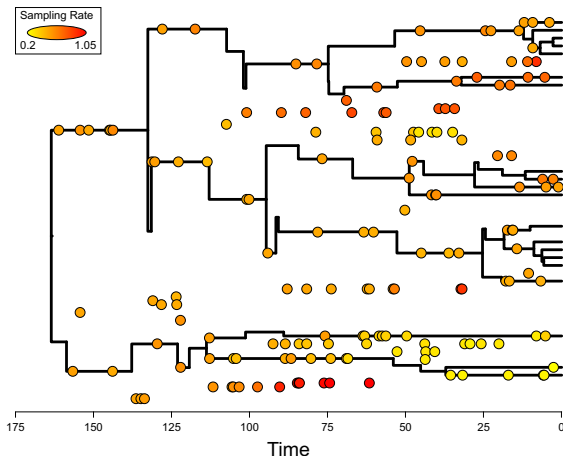
Sample the time from the MRCA to the fossil from a mixture of different exponential distributions

Account for uncertainty in values of λ



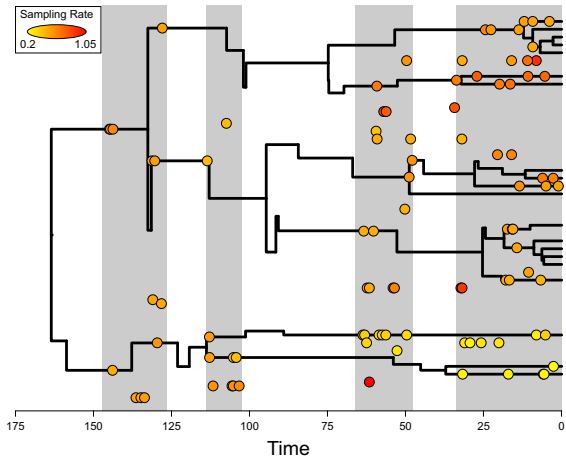
COMPLEX MODELS OF MACROEVOLUTION

Modeling
branching
patterns AND
fossilization,
preservation, and
recovery for use
as priors for
divergence time
estimation



COMPLEX MODELS OF MACROEVOLUTION

Incorporate more information from the fossil and rock records and construct better and more realistic tree priors



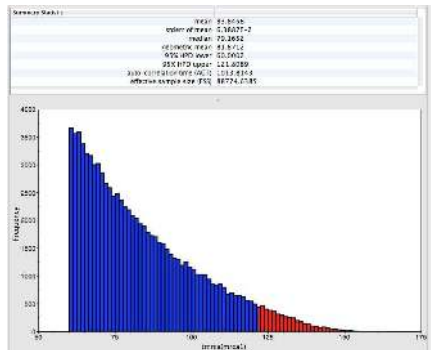
CRITICISM OF RELAXED CLOCK METHODS

- Dependent on and sensitive to fossil calibrations — fossil age estimates and node assignment are not without error
- Models are not biologically realistic
- Different methods/models can produce very different estimates of the same divergence times
- Priors are too informative
- Studies comparing methods have produced conflicting and unclear results

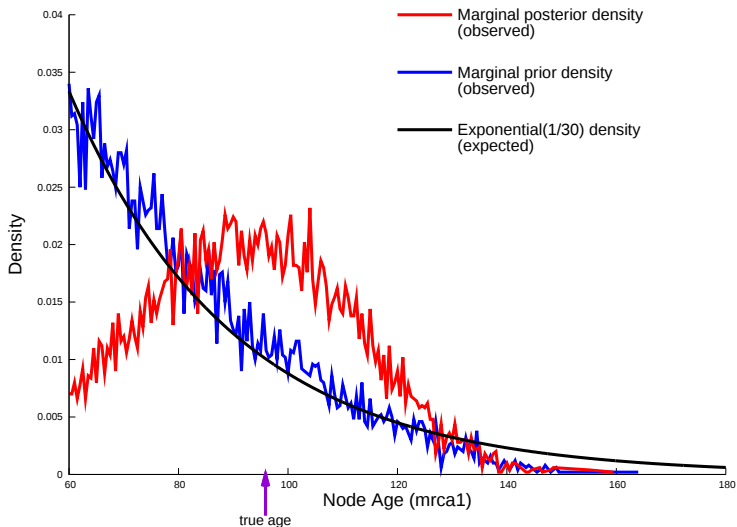
MCMC UNDER THE PRIOR

It is critical for any Bayesian analysis to sample under the prior

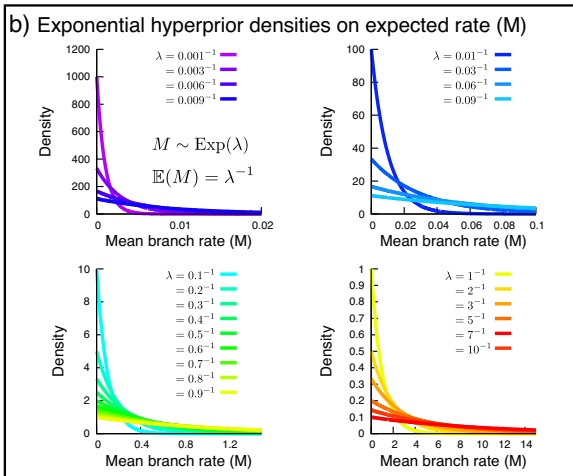
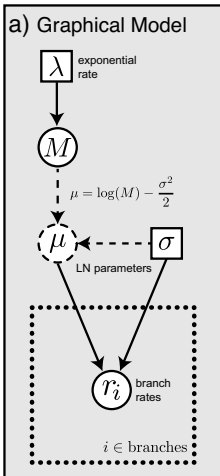
Allows you to assess your prior specification and examine prior sensitivity



MCMC UNDER THE PRIOR

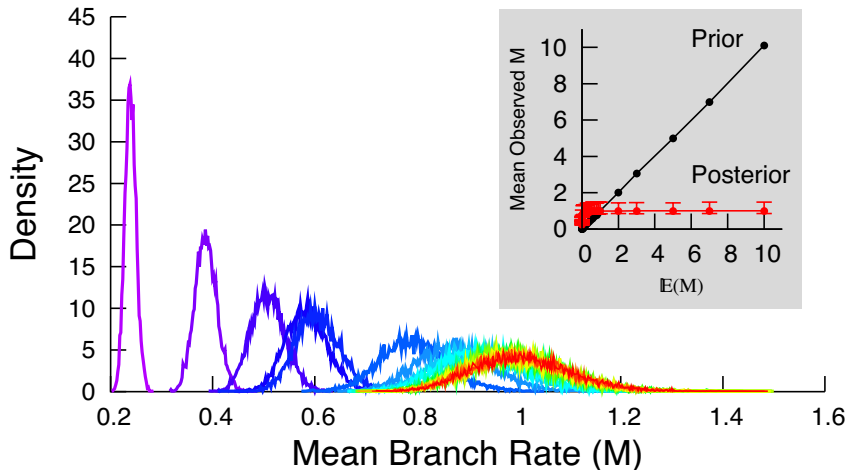


SENSITIVITY TO THE PRIOR

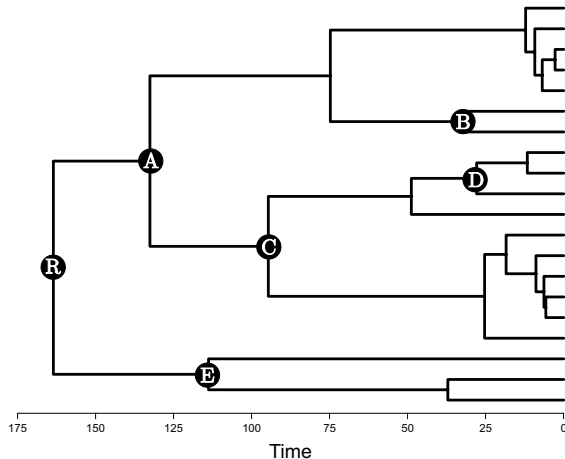


SENSITIVITY TO THE PRIOR

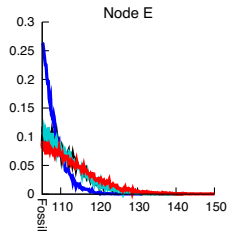
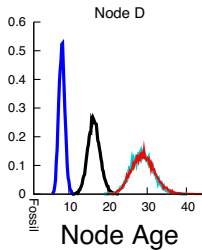
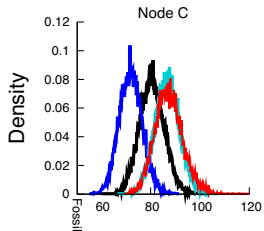
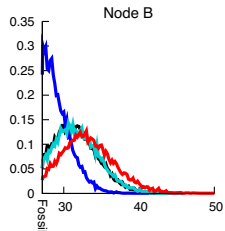
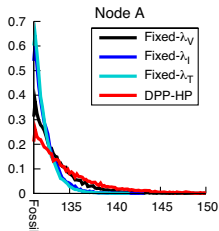
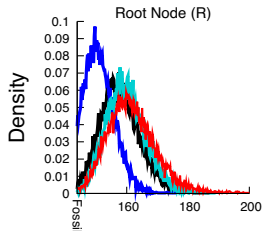
Marginal posterior densities of mean branch rate



CALIBRATED NODE AGE ESTIMATES



SENSITIVITY TO THE CALIBRATION PRIOR

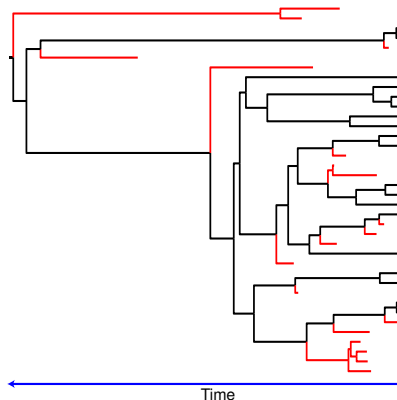


FOSSIL TIP DATING

Ideally, we would like to include all of the available data

Account for uncertainty in the placement of fossil lineages

Keep all fossil data, not just the oldest descendant for a given node

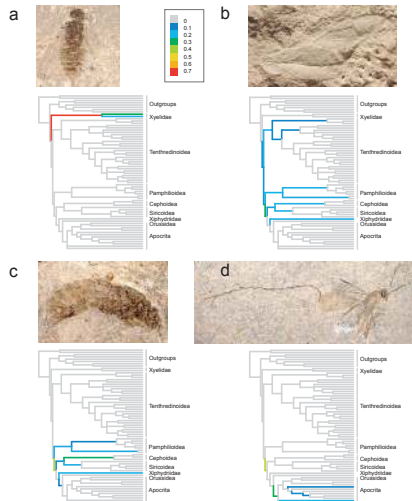


FOSSIL TIP DATING

Fredrik Ronquist and his colleagues implemented tip dating in MrBayes

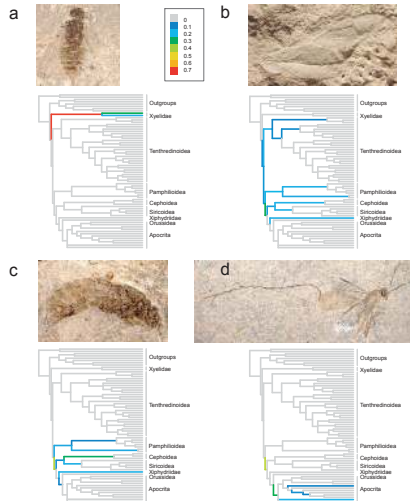
Early radiation of Hymenoptera

- 66 extant taxa
- 45 fossil taxa
- 7 genes, ~ 5kB (extant taxa only)
- 343 morphological characters (12% complete for fossils)



FOSSIL TIP DATING

- Hymenoptera fossils are mostly poorly-preserved impression fossils, difficult to place phylogenetically
- With node dating, their set of 45 fossils are reduced to 9 calibration points
- They developed a, presumably, vague uniform prior on node times

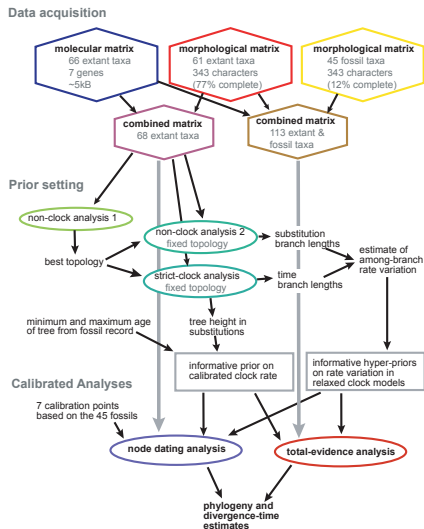


FOSSIL TIP DATING

Thorough analysis is necessary for this kind of dataset

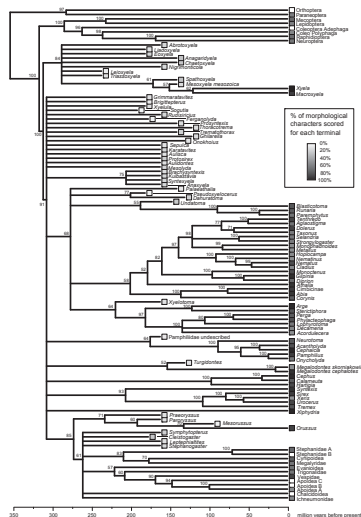
Ronquist et al. used Bayes factors to choose a relaxed clock model (this is rarely done, but really important)

Compared node dating and tip dating



FOSSIL TIP DATING

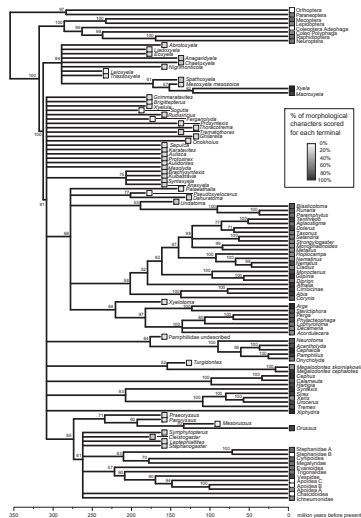
- Resulted in a fairly unresolved phylogeny, but fossils significantly contribute to estimates of node ages
- Posteriors on node times are less sensitive to priors compared with node dating
- Higher precision for divergence time estimates



FOSSIL TIP DATING

The Hymenoptera crown group dates back to the Carboniferous, approximately 309 Ma (95% interval: 291–347 Ma)

And diversified into major extant lineages much earlier than previously thought, well before the Triassic

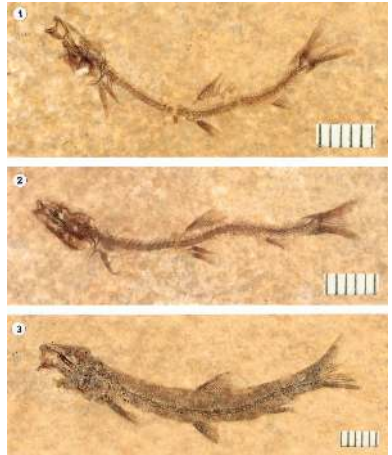


FOSSIL TIP DATING

In groups with rich fossil records, tip dating is an ideal approach

Allows for dating trees with more of the available fossils

Investigate questions (i.e. historical biogeography, character evolution) with extinct lineages



Notogoneus osculus — early growth series

illustrating the ontogeny of the scale covering

FOSSIL TIP DATING

Fossil tip-dating methods are available in MrBayes and BEAST, though our understanding of how well these methods work is still incomplete

